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OM protein - protein search, using sw model

Run on: August 19, 2004, 13:30:29 ; Search time 53 Seconds
 (without alignments)

836.980 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGLEKSLKSLVIRNLNDQVL.....LKKEDELGDRSIMFTVQNED 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	811	99.9	157	2	AAW77077	Human int
2	811	99.9	157	3	AAV57570	Human int
3	811	99.9	157	4	AAV57570	Human int
4	811	99.9	157	4	AAV57570	Human int
5	811	99.9	157	4	AAV57570	Human int
6	811	99.9	157	5	AAV57570	Human int
7	811	99.9	157	5	AAV57570	Human int
8	811	99.9	157	5	AAV57570	Human int
9	811	99.9	157	6	AAV57570	Human int
10	811	99.9	157	6	AAV57570	Human int
11	811	99.9	157	6	AAV57570	Human int
12	811	99.9	157	6	AAV57570	Human int
13	811	99.9	157	7	AAV57570	Human int
14	811	99.9	158	3	AAV57570	Human int
15	811	99.9	177	6	AAV57570	Human int
16	811	99.9	180	2	AAV57570	Human int
17	811	99.9	193	2	AAV57570	Human int
18	811	99.9	193	2	AAV57570	Human int
19	811	99.9	193	4	AAV57570	Human int
20	811	99.9	193	4	AAV57570	Human int
21	811	99.9	193	5	AAV57570	Human int
22	811	99.9	233	5	AAV57570	Human int
23	811	99.9	536	5	AAV57570	Human int
24	811	99.9	588	5	AAV57570	Human int
25	811	99.9	1048	5	AAV57570	Human int

26	810	99.8	157	2	AAV57570	Human int
27	810	99.8	157	2	AAV57570	Human int
28	810	99.8	157	2	AAV57570	Human int
29	810	99.8	157	2	AAV57570	Human int
30	810	99.8	157	2	AAV57570	Human int
31	810	99.8	157	2	AAV57570	Human int
32	810	99.8	157	2	AAV57570	Human int
33	810	99.8	157	2	AAV57570	Human int
34	810	99.8	157	2	AAV57570	Human int
35	810	99.8	157	2	AAV57570	Human int
36	810	99.8	157	2	AAV57570	Human int
37	810	99.8	157	2	AAV57570	Human int
38	810	99.8	157	2	AAV57570	Human int
39	810	99.8	157	2	AAV57570	Human int
40	810	99.8	157	2	AAV57570	Human int
41	810	99.8	157	2	AAV57570	Human int
42	810	99.8	157	2	AAV57570	Human int
43	810	99.8	157	2	AAV57570	Human int
44	810	99.8	157	2	AAV57570	Human int
45	810	99.8	157	2	AAV57570	Human int

ALIGNMENTS

RESULT 1	
AAW77077	
ID	AAW77077 standard; peptide; 157 AA.
XX	
AC	AAW77077;
XX	
DT	16-NOV-1998 (first entry)
XX	
DE	Human interleukin 18.
XX	
KW	Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
KW	osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
KW	chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.
XX	
OS	Homo sapiens.
XX	
PN	EP861663-A2.
XX	
PD	02-SEP-1998.
XX	
PF	24-FEB-1998;
XX	98EP-00301352.
PR	25-FEB-1997;
XX	97JP-00055468.
XX	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX	Gillespie MT, Horwood NJ, Udagawa N, Kurimoto M;
XX	WPI; 1998-448964/39.
XX	N-PSDB; AAV48226.
XX	
PT	Use of interleukin-18 to inhibit osteoclast formation - in treatment of
PT	e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome, osteosarcoma,
PT	chronic rheumatoid arthritis, deformity ostitis, primary hyperthyroidism
XX	and osteoporosis.
XX	Claim 4; Page 18; 56pp; English.
CC	Interleukin-18 (IL-18) or a functional equivalent can be used for
CC	inhibition of osteoclast formation. IL-18 is used for treating or
CC	preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
CC	Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
CC	arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
XX	osteoporosis
SQ	Sequence 157 AA;

Query Match 99.9%; Score 811; DB 2; Length 157;

Best Local Similarity 99.4%; Pred. No. 9.8e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTKSDIIFQRSVPGHDKMQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTKSDIIFQRSVPGHDKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 2

AA57570
ID AAY57570 standard; protein; 157 AA.

XX AC AAY57570;

XX DT 06-MAR-2000 (first entry)

XX DE Human interleukin 18 protein sequence SEQ ID NO:1.

XX KW Human; interleukin 18; IL-18; potentiators; IGIF; tumour; cancer;

XX KW interferon-gamma-inducing factor; growth inhibition; cytostatic.

XX OS Homo sapiens.

XX PN WO9959565-A1.

XX PD 25-NOV-1999.

XX PF 20-MAY-1999; 99WO-US011160.

XX PR 21-MAY-1998; 98US-0086560P.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Johnson RK;

XX PS WPI; 2000-062368/05.

XX PT New polypeptides, useful for preparation of composition for preventing and/or treating cancer by inhibiting tumor growth.

XX PS Claim 1; Page 49-50; 53pp; English.

XX CC The present sequence represents human interleukin 18 (IL-18). The present invention describes a compound comprising human or murine IL-18 in combination with a chemotherapeutic agent (1). Also described are: (1) a method of preventing and/or treating cancer in a mammal comprising the administration of a cancer inhibiting amount of (1) comprising the IL-18 protein and the chemotherapeutic agent and optionally a pharmaceutically acceptable carrier; and (2) a method of inhibiting the growth of tumour cells in a mammal sensitive to a composition comprising human IL-18 and/or murine IL-18 and the chemotherapeutic agent (and optionally a pharmaceutically acceptable carrier), comprising administering to a mammal afflicted with the tumour cells an effective tumour cell growth inhibiting amount of (1). The IL-18 protein in conjunction with a chemotherapeutic agent is useful in a method for preventing and/or treating cancer in mammals by inhibiting the growth of tumours or cancerous cells in mammals

XX SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 3; Length 157;

Best Local Similarity 99.4%; Pred. No. 9.8e-83;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60

DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTKSDIIFQRSVPGHDKMQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTKSDIIFQRSVPGHDKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 3

AAG65351

ID AAG65351 standard; protein; 157 AA.

XX AC AAG65351;

XX DT 30-NOV-2001 (first entry)

XX DE Human interleukin-18 (IL-18) protein fragment.

XX KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective; neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiac; immunosuppressive; antidepressant; neuroleptic; hepatotropic.

XX OS Homo sapiens.

XX PN WO200158956-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US004170.

XX PR 10-FEB-2000; 2000US-0181608P.

XX PA (BADI) BASF AG.

XX PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J, Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE, Lennard SN;

XX DR WPI; 2001-550020/61.

XX PT Novel antibodies and compounds capable of binding to human interleukin-18 useful for treating, e.g., inflammatory disorders, neurological disorders, heart failure, myocardial infarction, and autoimmune diseases.

XX PS Disclosure; Page 14; 91pp; English.

XX CC The invention provides isolated antibodies, or antigen-binding portions, that are capable of binding to human interleukin-18 (IL-18). The antibodies may be used to inhibit human IL-18 activity in, and treat a disorder where IL-18 is detrimental in, a human subject suffering from, inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease, inflammatory bowel disease, and osteoarthritis), neurological disorders (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and stroke), heart failure, myocardial infarction, autoimmune diseases such as autoimmune hepatitis and autoimmune neuropenia, and mental disorders (e.g., depression and schizophrenia). Treatment with an anti-IL-18 antibody may occur before, concurrent, or after administration of a second agent selected from an antibody, or fragment, capable of binding human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids, cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory agents. The present sequence represents a human IL-18 protein fragment

XX SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 4; Length 157;

Best Local Similarity 99.4%; Pred. No. 9.8e-83;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60

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Db      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFITISMYKDSQPRGM 60
Qy      61 AVTISVCKEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQPESSSY 120
Db      61 AVTISVCKEKISTSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQPESSSY 120
Qy      121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db      121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 4
AAG65294
ID      AAG65294 standard; protein; 157 AA.
XX
AC      AAG65294;
XX
DT      30-NOV-2001 (first entry)
XX
DE      Human interleukin-18 (IL-18) protein fragment.
XX
KW      IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW      nocropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW      immunosuppressive; antidepressant; neuroleptic; hepatotropic.
XX
OS      Homo sapiens.
XX
PN      WO200158956-A2.
XX
PD      16-AUG-2001.
XX
PF      09-FEB-2001; 2001WO-US004170.
XX
PR      10-FEB-2000; 2000US-0181608P.
XX
PA      (BADI ) BASF AG.
XX
PI      Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI      Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI      Lennard SN;
XX
DR      WPI; 2001-550020/61.
XX
PT      Novel antibodies and compounds capable of binding to human interleukin-18
PT      useful for treating e.g., inflammatory disorders, neurological
PT      disorders, heart failure, myocardial infarction, and autoimmune diseases.
XX
PS      Disclosure; Page 9; 91pp; English.
XX
CC      The invention provides isolated antibodies, or antigen-binding portions,
CC      that are capable of binding to human interleukin-18 (IL-18). The
CC      antibodies may be used to inhibit human IL-18 activity in, and treat a
CC      disorder where IL-18 is detrimental in, a human subject suffering from,
CC      inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC      inflammatory bowel disease, and osteoarthritis), neurological disorders
CC      (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC      stroke), heart failure, myocardial infarction, autoimmune diseases such
CC      as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
CC      (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC      antibody may occur before, concurrent, or after administration of a
CC      second agent selected from an antibody, or fragment, capable of binding
CC      human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC      cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC      agents. The present sequence represents a human IL-18 protein fragment
XX
SQ      Sequence 157 AA;
Query Match      99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 9.8e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFITISMYKDSQPRGM 60

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Db      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFITISMYKDSQPRGM 60
Qy      61 AVTISVCKEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQPESSSY 120
Db      61 AVTISVCKEKISTSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQPESSSY 120
Qy      121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db      121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 5
AAE06661
ID      AAE06661 standard; protein; 157 AA.
XX
AC      AAE06661;
XX
DT      16-OCT-2001 (first entry)
XX
DE      Human interleukin-1gamma (IL-1gamma) protein.
XX
KW      Human; interleukin-1gamma; IL-1gamma; virucide; hepatotropic; fever;
KW      immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
KW      autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
KW      psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
XX
OS      Homo sapiens.
XX
PN      WO200157219-A2.
XX
PD      09-AUG-2001.
XX
PF      01-FEB-2001; 2001WO-US003285.
XX
PR      02-FEB-2000; 2000US-0179638P.
XX
PA      (SCHE ) SCHERING CORP.
XX
PI      Debets JEMA, Timans JC, Bazan JF, Kastelein RA;
XX
DR      WPI; 2001-488886/53.
XX
PT      Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
PT      polypeptide useful for treating conditions exhibiting abnormal expression
PT      of interleukin such as immunological disorders, tumor and allergy.
XX
PS      Disclosure; Fig 1; 103pp; English.
XX
CC      The invention relates to recombinant antigenic interleukin-1 like
CC      molecules and their corresponding nucleic acid sequences, designated as
CC      interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon). IL
CC      -1delta and IL-1epsilon are useful for treating conditions exhibiting
CC      abnormal expression of the interleukin such as immunological disorders,
CC      tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
CC      allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
CC      tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
CC      HIV). The invention also relates to methods of using the composition
CC      containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
CC      utilities. IL-1delta is used as an immunogen for the production of
CC      antisera or antibodies specific, e.g., capable of distinguishing between
CC      IL-1 family members and an IL-1delta, for the interleukin or its
CC      fragment. The purified interleukin is used as a reagent to detect any
CC      antibodies generated in response to the presence of elevated levels of
CC      expression, or immunological disorders which lead to antibody production
CC      to the endogenous cytokine. The invention also contemplates the use of
CC      competitive drug screening assays. The present sequence is human
CC      interleukin-1gamma (IL-1gamma) protein related to the invention
XX
SQ      Sequence 157 AA;
Query Match      99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 9.8e-83;

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Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Qy 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQFESSY 120
Db 61 AVTISVKCEKISTUSCENKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 6
ABB04389
ID ABB04389 standard; protein; 157 AA.
XX
AC ABB04389;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human IL-18.
XX
KW Human; IL-18; interleukin-18; cancer.
XX
OS Homo sapiens.
XX
FN CN1326992-A.
XX
PD 19-DEC-2001.
XX
PF 07-JUN-2000; 2000CN-00107993.
XX
PR 07-JUN-2000; 2000CN-00107993.
XX
PA (SHUA-) SHUANGLU PHARM CO LTD BEIJING.
XX
PI Xu M, Wang Y, Huang X;
XX
DR WPI; 2002-217571/28.
XX
N-PSDB; ABL41315.
XX
PT Gene cloning, product preparation and use of Chinese interleukin-18
PT subtype (53 Arg IL-18), useful for treating of cancer and other disease.
XX
PS Claim 1; Page 7 (Disclosure); 8pp; Chinese.
XX
CC The invention relates to the preparation of recombinant human interleukin
CC -18 for treating of cancer and other disease
XX
SQ Sequence 157 AA;
Query Match 99.9%; Score 811; DB 5; Length 157;
Best Local Similarity 99.4%; Pred. No. 9.8e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Qy 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQFESSY 120
Db 61 AVTISVKCEKISTUSCENKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 7
AAE17134
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ID AAE17134 standard; protein; 157 AA.
XX
AC AAE17134;
XX
DT 22-APR-2002 (first entry)
XX
DE Human IL-18 protein.
XX
KW Human; viral disease; IL-18; interferon-gamma-inducing factor; IGIF; HSV;
KW influenza virus; human immunodeficiency virus; HIV; herpes simplex virus;
KW hepatitis A virus; HAV; hepatitis B virus; HBV; human papillomavirus;
KW HPV; hepatitis C virus; HCV.
XX
OS Homo sapiens.
XX
FN WO200193898-A1.
XX
PD 13-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US017924.
XX
PR 02-JUN-2000; 2000US-0208869P.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Esser KM, Rosenberg M, Tal-Singer R, Woodnutt G, Chisari FV;
XX
DR WPI; 2002-154554/20.
XX
PT Treatment of disease caused by e.g. influenza virus comprises
PT administration of composition containing polypeptide, having identity of
PT amino acid sequences.
XX
PS Claim 1; Fig 1; 4lpp; English.
XX
CC The invention relates to a method for treating viral diseases with IL-18,
CC also known as interferon-gamma-inducing factor (IGIF) and IL-18
CC combinations. The method involves administering a composition comprising
CC IL-18 and IL-18 in combination with other agents. The method is used for
CC treating diseases caused by viruses such as influenza virus, human
CC immunodeficiency virus (HIV), herpes simplex virus (HSV), hepatitis A
CC virus (HAV), hepatitis B virus (HBV), human papillomavirus (HPV) and
CC hepatitis C virus (HCV). The present sequence is human IL-18 protein
XX
SQ Sequence 157 AA;
Query Match 99.9%; Score 811; DB 5; Length 157;
Best Local Similarity 99.4%; Pred. No. 9.8e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Qy 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQFESSY 120
Db 61 AVTISVKCEKISTUSCENKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 8
AAE16954
ID AAE16954 standard; protein; 157 AA.
XX
AC AAE16954;
XX
DT 18-APR-2002 (first entry)
XX
DE Human active interleukin-18 (IL-18) protein.
XX
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KW Human; interleukin-18; IL-18; caspase; interferon gamma; IFN-gamma;
 KW immunocompetent.
 XX
 OS Homo sapiens.
 XX
 PN WO200198455-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 11-JUN-2001; 2001WO-US018804.
 XX
 PR 15-JUN-2000; 2000US-0211832P.
 PR 10-AUG-2000; 2000US-0224128P.
 PR 20-JAN-2001; 2001US-0264923P.
 XX
 PA (SMIK) SMITHLINE BEECHAM CORP.
 XX
 PI Johanson KO, Kirkpatrick RB, Shatzman AR, Hoy YS, Mcdevitt P;
 XX
 DR WPI; 2002-139786/18.
 XX
 PT Activation of precursor polypeptide e.g. interleukin-18 polypeptide
 PT useful for inducing interferon-gamma production, comprises contacting or
 PT co-expressing caspase 4 or caspase 5 with precursor polypeptide.
 XX
 PS Claim 9; Fig 3; 64pp; English.
 XX
 CC The invention relates to a method for the in vitro activation of human
 CC precursor interleukin-18 (Pro-IL-18) with an activating enzyme. The
 CC method comprises contacting precursor IL-18 with an activating enzyme
 CC such as caspase 4 or caspase 5. Caspases 4 and 5 are members of a family
 CC of cysteine proteases that include interleukin-1beta converting enzyme
 CC (ICE), which preferentially cleave substrates containing a protease
 CC activation motif. The methods are useful for producing physiologically
 CC active polypeptide e.g. active IL-18 polypeptide. The active IL-18
 CC polypeptide has an activity of inducing the production of interferon
 CC (IFN)-gamma in immunocompetent cells. IFN-gamma is useful as a
 CC biologically active substance for stimulating the production of IFNg from
 CC KG-1 (human myelomonocytic cell line) cells. The present sequence is
 CC human active IL-18 protein
 XX
 SQ Sequence 157 AA;
 Query Match 99.9%; Score 811; DB 5; Length 157;
 Best Local Similarity 99.4%; Pred. No. 9.8e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
 DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
 QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKOTKSDIIFQSVPGHDNKMOPESSY 120
 DB 61 AVTISVKCEKISTUSCEKNIISFKEMNPPDNKOTKSDIIFQSVPGHDNKMOPESSY 120
 QY 121 EGYFLACEKERDLFKLLILKKEDELGDRSIMFTVQNE 157
 DB 121 EGYFLACEKERDLFKLLILKKEDELGDRSIMFTVQNE 157
 RESULT 9
 ABG73359
 ID ABG73359 standard; protein; 157 AA.
 XX
 AC ABG73359;
 XX
 DT 13-MAY-2003 (first entry)
 XX
 DE Human wild-type mature interleukin-18 (IL-18).
 XX
 KW Human; human interleukin-18; IL-18; IL-18 binding protein; IL-18BP;
 KW T helper type I response; Th1 response; cancer; viral disease;
 KW microbial infection; tumour immunotherapy; adjuvant; DNA vaccination;

KW graft versus tumour therapy; neutralisation; cytostatic; virucide;
 KW antimicrobial.
 XX
 OS Homo sapiens.
 XX
 PN US2002169291-A1.
 XX
 PD 14-NOV-2002.
 XX
 PF 08-MAR-2002; 2002US-00094153.
 XX
 PR 08-MAR-2001; 2001US-0274327P.
 XX
 PA (DINA/) DINARELLO C.
 PA (KIMS/) KIM S H.
 XX
 PI Dinarello C, Kim SH;
 XX
 DR WPI; 2003-298731/29.
 DR N-PSDB; ABX11788.
 XX
 PT Novel interleukin-18 mutant polypeptide useful in the treatment of cancer
 PT and viral disease, has mutations in amino acid residues which are
 PT involved in its interaction with IL-18 binding protein.
 XX
 PS Example 1; Fig 1B; 23pp; English.
 XX
 CC The present invention relates to mutants of human interleukin-18 (IL-18)
 CC protein that have a lower affinity for IL-18 binding protein (IL-18BP)
 CC than the wild-type IL-18 protein. The IL-18 mutants of the invention
 CC comprise mutations in one or more amino acid residues which are involved
 CC in its interaction with IL-18BP. The mutations comprise substitutions,
 CC preferably non-conservative, additions or deletions. A pharmaceutical
 CC composition comprising an IL-18 mutant is useful for treating a disease
 CC which is prevented or alleviated by a T helper type I (Th1) response,
 CC including cancer and viral disease. The IL-18 mutants are useful in the
 CC treatment of the above diseases, microbial infections, in tumour
 CC immunotherapy, and as an adjuvant in DNA vaccination and in graft versus
 CC tumour therapy. The IL-18 mutants are resistant to, or less susceptible
 CC to, neutralisation than the wild-type protein. The present sequence
 CC represents human wild-type mature IL-18 protein
 XX
 SQ Sequence 157 AA;
 Query Match 99.9%; Score 811; DB 6; Length 157;
 Best Local Similarity 99.4%; Pred. No. 9.8e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
 DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
 QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKOTKSDIIFQSVPGHDNKMOPESSY 120
 DB 61 AVTISVKCEKISTUSCEKNIISFKEMNPPDNKOTKSDIIFQSVPGHDNKMOPESSY 120
 QY 121 EGYFLACEKERDLFKLLILKKEDELGDRSIMFTVQNE 157
 DB 121 EGYFLACEKERDLFKLLILKKEDELGDRSIMFTVQNE 157
 RESULT 10
 ADA50616
 ID ADA50616 standard; protein; 157 AA.
 XX
 AC ADA50616;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human mature consensus interleukin-18 (IL-18), SEQ ID NO:71.
 XX
 KW Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;
 KW humoral response; cellular response; immune response; immunotherapy;

protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
 111
 /note= "Lys may replace wild-type Asn in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
 129
 /note= "Phe may replace wild-type Lys in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
 131
 /note= "Asp may replace wild-type Arg in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
 132
 /note= "Leu may replace wild-type Asp in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
 133
 /note= "Glu may replace wild-type Leu in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
 134
 /note= "Ala may replace wild-type Phe in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"

WO2003031569-A2.

17-APR-2003.

18-SEP-2002; 2002WO-US029640.

10-OCT-2001; 2001US-0328371P.

(CENZ) CENTOCOR INC.

Snyder L, Scallion B, Knight DM, McCarthy SG, Goletz TJ; Branigan PJ;

WPI; 2003-393437/37.

N-PSDB; ADA50613.

New nucleic acid vaccine, useful for eliciting an immune response to a

Query Match 99.9%; Score 811; DB 6; Length 157;
 Best Local Similarity 99.4%; Pred. No. 9.8e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNKOTKSDIIFQRSVPVGHNDKMQPESSSY 120

Db 61 AVTISVKCEKISTLSCEKNKIIISFKEMNPPDNKOTKSDIIFQRSVPVGHNDKMQPESSSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIFMTVQNEH 157

Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIFMTVQNEH 157

RESULT 11

ADA50610 standard; protein; 157 AA.

XX AC ADA50610;

XX AC 20-NOV-2003 (first entry)

XX DT Human mature consensus interleukin-18 (IL-18), SEQ ID NO:65.

XX DE Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;

XX KW

KW humoral response; cellular response; immune response; immunotherapy;
 KW cancer; cytostatic; vaccine; gene therapy; interleukin-18; IL-18; human.
 XX Homo sapiens.
 OS WO2003031569-A2.
 PN 17-APR-2003.
 PD 18-SEP-2002; 2002WO-US029640.
 PF 10-OCT-2001; 2001US-0328371P.
 PR (CENZ) CENTOCOR INC.
 PA Snyder L, Scallion B, Knight DM, McCarthy SG, Goletz TJ;
 PI Branigan PJ;
 XX WPI; 2003-393437/37.
 DR N-PSDB; ADA50608.
 XX New nucleic acid vaccine, useful for eliciting an immune response to a
 PT cancer associated tumor protein in a mammal.
 FT Claim 1b; Page 51-52; 92pp; English.

The invention relates to a nucleic acid vaccine comprising one or more
 CC tumour antigen-encoding nucleic acids and one or more cytokine adjuvant-
 CC encoding nucleic acids. The tumour antigen encoded by the vaccine is
 CC mucin 1 (MUC-1), the kallikrein KKK2, or prostate specific antigen (PSA,
 CC also known as KLK3), and the cytokine adjuvant encoded can be interleukin
 CC -12 (IL-12), granulocyte macrophage-colony stimulating factor (GM-CSF),
 CC or especially interleukin-18 (IL-18). The antigen-encoding nucleic acid
 CC is preferably under the control of a promoter such as the cytomegalovirus
 CC immediate early promoter, the dihydrofolate reductase promoter or the
 CC early or late SV40 promoters. The invention also encompasses the method
 CC of eliciting an immune response to a tumour antigen in a mammal using the
 CC vaccine of the invention. Coexpression of the antigen and adjuvant
 CC induces a humoral or cellular response to the tumour antigen, generating
 CC an immune response useful for treatment or prophylaxis of cancers. The
 CC present sequence represents an interleukin-18 (IL-18) polypeptide which
 CC is specifically claimed for use in the vaccine of the invention.

Sequence 157 AA;

Query Match 99.9%; Score 811; DB 6; Length 157;
 Best Local Similarity 99.4%; Pred. No. 9.8e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNKOTKSDIIFQRSVPVGHNDKMQPESSSY 120

Db 61 AVTISVKCEKISTLSCEKNKIIISFKEMNPPDNKOTKSDIIFQRSVPVGHNDKMQPESSSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIFMTVQNEH 157

Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIFMTVQNEH 157

RESULT 12

ABR83372 standard; protein; 157 AA.

XX AC ABR83372;

XX AC 07-OCT-2003 (first entry)

XX DT Human interleukin 18 amino acid sequence.

XX DE Human; interleukin 1; IL-1; interleukin 18; IL-18; mutant; mutein;

XX KW

KW mutant interleukin 18; MUT-IL-18; antiinflammatory; gene therapy;
KW inflammatory disorder.

XX Homo sapiens.

XX WO2003057821-A2.

XX 17-JUL-2003.

XX 25-OCT-2002; 2002WO-US034235.

XX 26-OCT-2001; 2001US-0335880P.

XX (CENZ) CENTOCOR INC.

XX Heavner GA, Snyder LA, Mccarthy SG;

XX WPI; 2003-577517/54.

XX New MUT-IL-18 nucleic acid, useful for preparing a composition for
PT diagnosing or treating a MUT-IL-18 related condition, e.g., inflammatory
PT disorder.

XX Example 3; Page 74; 97pp; English.

CC The present invention describes a mutant interleukin 18 (MUT-IL-18)
CC nucleic acid comprising or complementary to at least one polynucleotide
CC encoding an IL-18 amino acid sequence comprising at least one mutation
CC corresponding to at least one substitution selected from the group
CC consisting of Thr10 for Ser10, Val12 for Ile12, Ser45 for Thr47
CC for Phe47, Phe52 for Tyr52, Val64 for Ile64, Tyr101 for Phe101, Val15 for
CC Leu5, Val20 for Leu20, Ile20 for Leu20, Tyr21 for Phe21, Val22 for Ile22,
CC Ile66 for Val66, Thr72 for Ser72, or Phe48 for Ser148. Also described:
CC (1) a MUT-IL-18 polypeptide; (2) a MUT-IL-18 antibody; (3) a MUT-IL-18
CC vector comprising the MUT-IL-18 nucleic acid; (4) a MUT-IL-18 host cell
CC comprising the MUT-IL-18 nucleic acid; (5) a composition comprising a MUT
CC -IL-18 nucleic acid, polypeptide or antibody; (6) diagnosing or treating
CC a MUT-IL-18 related condition in a cell, tissue, organ or animal; (7) a
CC device comprising MUT-IL-18 nucleic acid, polypeptide or antibody and
CC that is suitable for contacting or administering the MUT-IL-18 nucleic
CC acid, polypeptide or antibody; (8) an article of manufacture for human
CC pharmaceutical or diagnostic use; and (9) producing the MUT-IL-18 nucleic
CC acid, polypeptide or antibody. MUT-IL-18 has antiinflammatory activity
CC and can be used in gene therapy. The MUT-IL-18 has antiinflammatory activity
CC for preparing a composition for diagnosing or treating a MUT-IL-18
CC related condition, e.g., inflammatory disorder. The present sequence
CC represents a human IL-18 amino acid sequence given in an example from the
CC present invention

XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 6; Length 157;

Best Local Similarity 99.4%; Pred. No. 9.8e-83;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIKDKTSIIFFQSRVPGHDNKMQPESSSY 120

Db 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIKDKTSIIFFQSRVPGHDNKMQPESSSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEQ 157

Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEQ 157

RESULT 13

ADE06775

ID ADE06775 standard; protein; 157 AA.

XX

AC ADE06775;

XX 29-JAN-2004 (first entry)

XX Human anti-diabetes Ig derived protein SEQ ID NO:3.

XX human; Ig; diabetes; complementarity-determining region; CDR;

XX antidiabetic; ophthalmological; neuroprotective; gene therapy;

XX diabetes mellitus; insulin resistance; hyperglycaemia; hypoglycaemia;

XX pancreatitis; Cushing's syndrome; acanthosis nigricans; retinopathy;

XX nephropathy; polyneuropathy; ulcer; infection.

XX Homo sapiens.

XX WO2003083071-A2.

XX 09-OCT-2003.

XX 26-MAR-2003; 2003WO-US009459.

XX 26-MAR-2002; 2002US-0367902P.

XX (CENZ) CENTOCOR INC.

XX Griswold DE, Li J, Li L;

XX WPI; 2003-804047/75.

XX New isolated anti-diabetes immunoglobulin (Ig)-derived protein,
PT comprising at least one complementarity determining region (CDR) useful
PT for treating a diabetes-related condition, e.g. type I or II diabetes
PT mellitus, retinopathy.

XX Claim 1; SEQ ID NO 3; 84pp; English.

XX The invention relates to a novel isolated anti-diabetes immunoglobulin
CC (Ig)-derived protein, comprising at least one complementarity-determining
CC region (CDR). A protein of the invention has antidiabetic.

CC ophthalmological, and neuroprotective activity, and may have a use in

CC gene therapy. The protein, nucleic acid, composition and methods of the

CC invention are useful for treating a diabetes-related condition, e.g. type

CC I or II diabetes mellitus, insulin resistance, hyperglycaemia,

CC hypoglycaemia, pancreatitis, Cushing's syndrome, acanthosis nigricans,

CC retinopathy, nephropathy, polyneuropathy, ulcers, or infections. The

CC present sequence represents an anti-diabetes Ig derived protein of the

CC invention.

XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 7; Length 157;

Best Local Similarity 99.4%; Pred. No. 9.8e-83;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIKDKTSIIFFQSRVPGHDNKMQPESSSY 120

Db 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIKDKTSIIFFQSRVPGHDNKMQPESSSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEQ 157

Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEQ 157

RESULT 14

AAY85167

ID AAY85167 standard; protein; 158 AA.

XX

AC AAY85167;

XX 23-JUN-2000 (first entry)

XX


```
DE Human interleukin-18 (IL-18) amino acid sequence.
XX
XX Interleukin-18; production; IL-18; human; medical injection product.
XX
XX Homo sapiens.
XX
XX CN1243130-A.
XX
XX 02-FEB-2000.
XX
XX 24-JUL-1998; 98CN-00103307.
XX
XX 24-JUL-1998; 98CN-00103307.
XX
XX (WUGG/) WU G.
XX
XX Wu G, Liu Z;
XX
XX WPI; 2000-340020/30.
XX
XX N-PSDB; AAA10526.
XX
XX Preparation method for engineering bacteria for recombination of human
XX leucocyte medium-18 and its product thereof.
XX
XX Claim 1; Page 2; 17pp; English.
XX
XX This sequence represents the human interleukin-18 (IL-18) amino acid
XX sequence. The invention relates to a method for engineering bacterium for
XX recombination of human IL-18 and a method for the preparation of IL-18. A
XX primer containing a restriction endonuclease site can be used to
XX accurately obtain the IL-18 gene containing 474 nucleotides, and uses the
XX stop codon preferred by coli bacillus to raise the expression rate. The
XX method uses a high-amplification culture medium to increase the
XX expression level and only requires a one-step purification process to
XX obtain a medical injection-pure product
XX
XX Sequence 158 AA;
XX
XX Query Match 99.9%; Score 811; DB 3; Length 158;
XX Best Local Similarity 99.4%; Pred. No. 9.9e-83;
XX Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
XX 2 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 61
XX
XX 61 AVTISVKCEKISXLSCEENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHNDKMQFESSY 120
XX 62 AVTISVKCEKISXLSCEENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHNDKMQFESSY 121
XX
XX 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
XX 122 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 158
XX
XX RESULT 15
XX ADA50614
XX ID ADA50614 standard; protein; 177 AA.
XX
XX AC ADA50614;
XX
XX 20-NOV-2003 (first entry)
XX
XX Mature consensus IL-18/ILC signal sequence fusion protein, SEQ ID NO:69.
XX
XX Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;
XX humoral response; cellular response; immune response; immunotherapy;
XX cancer; cytostatic; vaccine; gene therapy; interleukin-18; IL-18; human.
XX
XX Chimeric.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX
```

```
FT Peptide 1..20
FT /label= Human_LC_signal_sequence
FT Protein 21..177
FT /label= Mature_consensus_IL-18
XX
XX WO2003031569-A2.
XX
XX 17-APR-2003.
XX
XX 18-SEP-2002; 2002WO-US029640.
XX
XX 10-OCT-2001; 2001US-0328371P.
XX
XX (CENZ ) CENTOCOR INC.
XX
XX Snyder L, Scallion B, Knight DM, Mccarthy SG, Goletz TJ;
XX Branigan PJ;
XX
XX WPI; 2003-393437/37.
XX
XX N-PSDB; ADA50611.
XX
XX New nucleic acid vaccine, useful for eliciting an immune response to a
XX cancer associated tumor protein in a mammal.
XX
XX Claim 1b; Page 53; 92pp; English.
XX
XX The invention relates to a nucleic acid vaccine comprising one or more
XX tumour antigen-encoding nucleic acids and one or more cytokine adjuvant-
XX encoding nucleic acids. The tumour antigen encoded by the vaccine is
XX mucin 1 (MUC-1), the kallikrein KUK2, or prostate specific antigen (PSA,
XX also known as KLK3), and the cytokine adjuvant encoded can be interleukin
XX -12 (IL-12), granulocyte macrophage-colony stimulating factor (GM-CSF),
XX or especially interleukin-18 (IL-18). The antigen-encoding nucleic acid
XX is preferably under the control of a promoter such as the cytomegalovirus
XX immediate early promoter, the dihydrofolate reductase promoter or the
XX early or late SV40 promoters. The invention also encompasses the method
XX of eliciting an immune response to a tumour antigen in a mammal using the
XX vaccine of the invention. Coexpression of the antigen and adjuvant
XX induces a humoral or cellular response to the tumour antigen, generating
XX an immune response useful for treatment or prophylaxis of cancers. The
XX present sequence represents an interleukin-18 (IL-18) polypeptide which
XX is specifically claimed for use in the vaccine of the invention.
XX
XX Sequence 177 AA;
XX
XX Query Match 99.9%; Score 811; DB 6; Length 177;
XX Best Local Similarity 99.4%; Pred. No. 1.2e-82;
XX Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
XX 21 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 80
XX
XX 61 AVTISVKCEKISXLSCEENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHNDKMQFESSY 120
XX 81 AVTISVKCEKISXLSCEENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHNDKMQFESSY 140
XX
XX 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
XX 141 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 177
XX
XX Search completed: August 19, 2004, 13:35:04
XX Job time : 54 secs
XX
```

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A;Gene: SPDB:SPBC3B9.02c

A,Map position: 2

Query Match 10.5%; Score 85; DB 2; Length 381;
Best Local Similarity 26.4%; Pred. No. 1.6;
Matches 39; Conservative 23; Mismatches 54; Indels 32; Gaps 7;
QY 3 GKLESKLVIRNLNDQVLFDIQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMV 62
DB 208 QQLSSKDAF--DVNQRPFLGMAKPVDSSELTFLDIWKNPKTMF----- 250
QY 63 TISVK-CEKISKLSKSCENKIISF-KEMNPPDNIKDKSDIIFQRSVPGHDKMOPFESSY 120
DB 251 -LPVKPLESSNALNSQNEHTEVQKKSNSIDNL--TPSSSELPKRS---RDNNLSRESS-- 302
QY 121 EGYFLACEKERDLFKLILKKEDELGDRS 148
DB 303 -----VSSKHLIDYNSRNTNKRDRDPRT 325
RESULT 3
T39487
hypotheical protein SPBC15D4.11c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C:Accession: T39487
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gaillardin, C.
submitted to the EMBL Data Library, August 1997
A:Reference number: 221858
A:Accession: T39487
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-263 <LYN>
A:Cross-references: EMBL:AL031349; PIDN:CAA20486.2; GSPDB:GN00067; SPDB:SPBC15D4.11c
A:Experimental source: strain 972h; cosmid c15D4
C:Genetics:
A:Gene: SPDB:SPBC15D4.11c
A:Map position: 2
A:Introns: 96/2; 147/3
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC15D4.11c

Query Match 10.1%; Score 82; DB 2; Length 263;
Best Local Similarity 21.7%; Pred. No. 2;
Matches 35; Conservative 33; Mismatches 65; Indels 28; Gaps 5;
QY 4 KLESKLVIRNLNDQVLFDIQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMV 63
DB 47 KLDSELGVYKQVLDLTPKKGYEKALHSFIHED-----PSLNYISALKETAKERIRVT 100
QY 64 ISVCKEKISKLSKSCENKIISFKEMNPPDNIKDKSDIIFQRSVPGH----- 109
DB 101 VPVYSSRSKYV--QTKPIITHGAEN--ENGNETSDSELVFFQHSIPAYVQLTNNHGTILCAL 156
QY 110 ---DNKMOPFESSSYEGYFLACEKERDLFKLILKKEDELGDR 147
DB 157 ILCKGMHLHFDSTISFQSPQNSQAFSSDL-RLIILQKSQKVTGR 196

RESULT 4
S10532
interleukin-1 alpha precursor - pig
N:Alternate names: hematopoietin-1; IL-1 alpha
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 20-Feb-1995 #sequence_revision 22-Nov-1996 #text_change 28-Jan-2000
C:Accession: S10532
R:Maliszewski, C.R.; Renshaw, B.R.; Schoenborn, M.A.; Urban, J.F.; Baker, P.E.
Nucleic Acids Res. 18, 4282, 1990
A:Title: Porcine IL-1 alpha cDNA nucleotide sequence.
A:Reference number: S10532; MUID: 90332454; PMID: 2377484
A:Accession: S10532
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-270 <MAL>
A:Cross-references: EMBL:X52731; NID:g1987; PIDN:CAA36945.1; PID:g1988

C;Comment: Produced by activated macrophages, the IL-1 proteins stimulate thymocyte proliferation.
C;Comment: IL-1 proteins are involved in the inflammatory response, being identified as a form of interleukin-1alpha, unlike interleukin-1beta, is fully active.

C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage
F:113-270/Product: interleukin-1 alpha #status predicted <PRO>
F:82.83/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 10.0%; Score 81.5; DB 1; Length 270;
Best Local Similarity 22.7%; Pred. No. 2.3;
Matches 30; Conservative 32; Mismatches 57; Indels 13; Gaps 6;
QY 8 KLSVIRNLNDQVLFDIQGNRPLFEDMTD-----SDCRDNAPRTI-FIISMYKDSQPRGMV 62
DB 123 KYNFWRVINHQICILNDARNQSIIRDPSQYLMAAVLNLDNAVKEDMAAYTSNDDSQLPV 182
QY 63 TISVKCEKISKLSKSCEN--KIISFKEM-NPPDNIKDKSDIIFQRSVPGHDKMOPFESS 119
DB 183 TLRIS-ETRLFVSAQNEDEPVLKELPETPKTIKDETSLLPFEWK---HGMNDYFKSAA 237
QY 120 YEGYFLACEKER 131
DB 238 HPKLFIAITROEK 249

RESULT 5
C71509
probable DNA polymerase I - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C:Accession: C71509
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: C71509
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-866 <ARN>
A:Cross-references: GB:AE001322; GB:AE001273; NID:g3328916; PIDN:AAC68093.1; PID:g3328922
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: polA
C:Superfamily: DNA-directed DNA polymerase I

Query Match 9.9%; Score 80.5; DB 2; Length 866;
Best Local Similarity 26.4%; Pred. No. 11;
Matches 34; Conservative 22; Mismatches 28; Indels 45; Gaps 8;
QY 1 YFGKLESKLVIRNLNDQVLFI---DQGNRPLFEDMTD-----SDCRDNAPRTIFI 49
DB 441 YFGMLASKLAIKN-----YLFVKLEEKGLKIDIFETVEQPLEAVLFAMEC-----V 486
QY 50 SMYKDSQPRGMV---TISVKCEKIS-----XLSCEKNIISFKEMN-----PPDN 91
DB 487 GMPLDQ--GLAVLDRLITKELECSQEIYDLVGCEFNKSPKQLSDILYQRLGIEPVDK 544
QY 92 IKOTKSDII 100
DB 545 AKSTKAEVL 553

RESULT 6
D64583
hypotheical protein HP0508 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C:Accession: D64583
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenna, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.

A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: D64583

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-452 <TOM>

A:Cross-references: GB:AE000565; GB:AE000511; NID:92313616; PIDN:AAD07578.1; PID:9231362

Query Match 9.7%; Score 79; DB 2; Length 452;
Best Local Similarity 23.8%; Pred. No. 7.4;
Matches 40; Conservative 30; Mismatches 72; Indels 26; Gaps 8;

Qy 9 LSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSOPR----- 58
Db 105 LVYFRQFNQA-FLIAPNDELYEQIRATNTDINFISDLLVTLFGDFPKIANLRKACNV 163

Qy 59 -GMATVISVCKEISLSCEN-KIISFKEMNPPDNIKDTSIIFFORSVPGHD----NK 112
Db 164 YSVGVYIVVTNINLISCFEILEKREL---DTSGVTKSTPFSR-VEGIDAGTLGK 219

Qy 113 MOPESSSYEGYF---LACEKRDLFKILKKEDELGDRSIMFTVQNE 156
Db 220 L-FSGSQSKNFAYVDALVKKKREKREIKKREIKDSIKREIKQE 266

RESULT 7
T44357
hypothetical protein [imported] - Clostridium histolyticum
C:Species: Clostridium histolyticum
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44357
R:Matsushita, O.; Jung, C.M.; Katayama, S.; Minami, J.; Takahashi, Y.; Okabe, A. J. Bacteriol. 181, 923-933, 1999
A:Title: Gene duplication and multiplicity of collagenases in Clostridium histolyticum.
A:Reference number: 222752; MUID:99121032; PMID:9922257
A:Accession: T44357
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-204 <MAT>
A:Cross-references: EMBL:AB014075; NID:93868863; PIDN:BAA34544.1; PID:93892648
A:Experimental source: strain JCM 1403

Query Match 9.7%; Score 78.5; DB 2; Length 204;
Best Local Similarity 26.4%; Pred. No. 3.2;
Matches 32; Conservative 19; Mismatches 51; Indels 19; Gaps 5;

Qy 9 LSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSOPRGMATVTSV 66
Db 25 ISTFENRHHKASSNKQGAKEKIN-----IDNSNSIKIVESVILKPEGEONKTTVDE 80

Qy 67 KCEK-----ISLSCENKIISFKEMNPPDNIKDTSIIFFORSVPGHNMKFSSS 119
Db 81 CIEKFNKDKVSDMTKEQVLAVFKKH--YNLKDIKDQIVFSRSI----NKYKYQEGK 134

Qy 120 Y 120
Db 135 Y 135

RESULT 8
T32038
hypothetical protein F41B5.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 16-Feb-2001
C:Accession: T32038
R:Dante, M.; Kramer, J.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of *C. elegans* cosmid F41B5.
A:Reference number: Z21115

A:Accession: T32038
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-473 <DAN>
A:Cross-references: EMBL:AF016676; PIDN:AAC25900.1; GSPDB:GN00023; CESP:F41B5.2
A:Experimental source: strain Bristol N2; clone F41B5
C:Genetics:
A:Gene: CESP:F41B5.2
A:Map position: 5
A:Introns: 67/1; 233/2; 403/3
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: heme; iron; metalloprotein
F:298-461/Domain: cytochrome P450 homology <P45>
F:439/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 9.6%; Score 78; DB 2; Length 473;
Best Local Similarity 21.5%; Pred. No. 9.7;
Matches 32; Conservative 28; Mismatches 57; Indels 32; Gaps 6;

Qy 10 SVIRNLNDQVLF---IDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSOPRGMATVTSV 66
Db 170 NAIANVINQITIFGYRFDSDNQBEYKCLKH-----LIEFQENVFTSAKVTVQV 216

Qy 67 KCEKISLSCENKIISFKEMNPPDNIKDTSIIFFORSVPGHNMKFSSSYEGYPL 125
Db 217 FAPKL-----GKILPGESLE--DLMKDWKNSFYDFNTQIENHRQKIDFDSSESQDYAE 268

Qy 126 ACEKRDLFKILKKEDELGDRSIMFTVQ 154
Db 269 AYLKEQ-----KKYEALGDTLFSNKQ 290

RESULT 9
A56677
neuronal cell cycle withdrawal protein QN1 - quail (fragment)
C:Species: Coturnix coturnix (quail)
C:Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Jul-2000
C:Accession: A56677
R:Bidou, L.; Crisanti, P.; Blancher, C.; Peseac, B. Mech. Dev. 43, 159-173, 1993
A:Title: A novel cDNA corresponding to transcripts expressed in retina post-mitotic neurogenesis.
A:Reference number: A56677; MUID:94128599; PMID:8297788
A:Accession: A56677
A:Molecule type: mRNA
A:Residues: 1-1251 <BID>
A:Cross-references: GB:S68151; NID:9545153; PIDN:AAD14007.1; PID:94261707
A:Note: conceptual translation not given

Query Match 9.5%; Score 77.5; DB 2; Length 1251;
Best Local Similarity 23.5%; Pred. No. 34;
Matches 38; Conservative 37; Mismatches 64; Indels 23; Gaps 9;

Qy 6 ESKLSVI--RNNDQVLF---DQGNRPLFEDMTSDCRDNAPRTFIISMYKDSOPRGMATVTSV 61
Db 648 EEKLAQIKEMEDQEVIIQGYQOENRKYKQMKDLQIQNKKEE---QMYKENQCL-MS 702

Qy 62 VTISVKCEKISLSCENKIISFKEMNPPDNIKDTSIIFFORSVPGHNMKFQFE----- 116
Db 703 ELIALR-EKVERINQSQIV--RESEPARN--QSFTELSLRLAARKSETKLUREIRLUK 757

Qy 117 -SSSYEGYFLACEKERDLFKILKKEDELGDRSIMFTVQNE 156
Db 758 QDKQALELDLQGAQKVERDLAKVQITSTS--SEKSYEFKIME 797

RESULT 10
A81261
probable periplasmic protein Cj1643 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C:Accession: A81261
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillingworth, N.; Bowden, J.; Brown, S.; Chillingworth, N.; Churcher, C.; De Lencastre, E.; et al. Nature 413, 84-88, 2001

Db 11 GRSDADLVFLNLTSPFDQNLQOQVLIKEIKKQLCEVQHERRC----- 54
Qy 55 SQRPRGMAVTISVKCKISKXLSKCNKIISFKEMNPPDNIKDTKSDII----- 100
Db 55 -----GVKFEVSLRSPNSALSFK-LSAPDLKEVKFDFVLPAYDLLDHLNLIKK 103
Qy 101 -----FFQR---SVP-GHDNKMQFESSYEGYFLACE--KERDLFKLI-----LKKEDBLG 145
Db 104 PNOQFYANLISGVPAGKEGKLSICFMGLQKQYFLNCRPTKLKRLIRLVTHWYQLCKE-KLG 162
Qy 146 D 146
Db 163 D 163

RESULT 14

I46620
interleukin-1 alpha precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 04-Feb-2000
C:Accession: I46620
R:Maliszewski, C.
Nucleic Acids Res. 14, 4282, 1990
A:Title: Nucleotide sequence of porcine interleukin-1 alpha.
A:Reference number: I46620
A:Accession: I46620
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-270 <MAL>
A:Cross-references: GB:M86730; NID:g164622; PIDN:AAA73198.1; PID:g164623
C:Superfamily: interleukin-1
E:Keywords: lipoprotein; myristylation
E:1-112/Domain: propeptide #status predicted <PRO>
E:113-270/Product: interleukin-1 alpha #status predicted <IL1>
F:82.83/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 9.3%; Score 75.5; DB 2; Length 270;
Best Local Similarity 22.0%; Pred. No. 8.7;
Matches 29; Conservative 32; Mismatches 58; Indels 13; Gaps 6;

Qy 8 KLSVIRNLNDQVLFDQGNRPLFEDMTD-----SDCRDNAPRTI-FIISMYKDSQPRGMAY 62
Db 123 KYNFMRVINHCILNDARNQSIIRDPSGQYLMAAVLNLDKAVKFDMAAYTSNDDSQLPV 182
Qy 63 TISVKCEKISXLSKCN--KISFKEM-NPPDNIKDTKSDIIFFQSRVPGHDKMKQFESS 119
Db 183 TLIRIS-ETRLFVSAQNEDEPVLLKELPPTKTIKDSLLPFWEK-----HGNMDYFKSAA 237
Qy 120 YEGYFLACEKER 131
Db 238 HPKLLIATRQEK 249

RESULT 15

H64245
hypothetical protein MG414 - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 02-Mar-2001
C:Accession: H64245; G64245
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: H64245
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1036 <TIGR>
A:Cross-references: GB:U39727; GB:L43967; NID:g1046127; PID:g1046129; TIGR:MG414
A:Experimental source: strain G-37
A:Accession: G64245

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 'M', 310-1036 <TIG2>
A:Cross-references: GB:U39727; GB:L43967; NID:g1046127; PID:g1046128; TIGR:MG413
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3
A:Start codon: GTG
C:Superfamily: hypothetical protein MG413

Query Match

Best Local Similarity 9.3%; Score 75.5; DB 2; Length 1036;
Matches 33; Conservative 32; Mismatches 65; Indels 21; Gaps 6;

Qy 14 NLNDQVLFIDQGNRPLFED--MTDSDCRDNAPRTIFIISMYKDSQPRGMAYTISVKCEK- 70
Db 845 SLNDEQLLVKLNITLSEKRLQTTKNVFNKKNKFNHILVENKKNQFNLFVDVDRSKL 904
Qy 71 ISXLSKCNKIISFKEMNPPDNIKDTKSDIIFFQSRVPGHDKMKQFESSYEGYFLACEK 129
Db 905 FIGVWVNDNQVFSISY-----DLKITNQTLIV-DANGFONSIFWFDITS-----EN 950
Qy 130 ERDLFKLI---LKKEDLGDRLSMTVQNE 157
Db 951 QTQLFKALSFYLNKNNLQFKRVPDFNLKSQD 981

Search completed: August 19, 2004, 13:36:45

Job time : 17 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 19, 2004, 13:31:14 ; Search time 13 Seconds
(without alignments)
628.847 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESLKSVIRNLNDQVL.....LKKEDELGRSIFMTVQNED 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	811	99.9	193	1	IL18_HUMAN	Q14116 homo sapien
2	659	81.2	193	1	IL18_HORSE	Q9xsg7 equus caball
3	654	80.5	193	1	IL18_BOVIN	Q9tu73 bos taurus
4	637	78.4	192	1	IL18_PIG	Q19073 sus scrofa
5	613	75.5	193	1	IL18_CANFA	Q9xsr0 canis famill
6	515	63.4	192	1	IL18_MOUSE	P70380 mus musculus
7	514.5	63.4	194	1	IL18_RAT	P97636 rattus norv
8	178.5	22.0	196	1	IL18_CHICK	Q8qf98 gallus gall
9	88	10.8	4705	1	FAT2_DROME	Q9vw71 drosophila
10	81.5	10.0	270	1	IL1A_PIG	P18430 sus scrofa
11	81	10.0	267	1	IL1A_RABIT	P04822 oryctolagus
12	80	9.9	1449	1	DP03_CLOPE	Q8xj33 clostridium
13	79.5	9.8	664	1	DNAK_CHLCV	Q824b2 chlamydomphi
14	77.5	9.5	674	1	MUTL_CLOPE	Q8x186 clostridium
15	76.5	9.4	270	1	IL1A_HORSE	Q60856 equus caball
16	75.5	9.3	192	1	OAGB_MOUSE	Q60856 mus musculus
17	75.5	9.3	1036	1	Y414_MYCGE	P47653 mycoplasma
18	75.5	9.3	1663	1	CO3_MOUSE	P01027 mus musculus
19	74.5	9.2	1228	1	EM14_HUMAN	Q13201 homo sapien
20	74	9.1	467	1	M3X8_MOUSE	Q07174 mus musculus
21	74	9.1	467	1	M3X8_RAT	Q63562 rattus norv
22	74	9.1	1772	1	MSP1_PLAYO	P13828 plasmodium
23	73	9.0	270	1	IL1A_PELCA	Q46613 felis silve
24	73	9.0	418	1	SYS_UREPA	Q9pr38 ureaplasma
25	73	9.0	426	1	YKXC_ASTLO	P51511 astasca lon
26	72.5	8.9	313	1	CO14_ARATH	Q9m9b3 arabidopsis
27	72.5	8.9	412	1	UVSE_CLOPE	Q8xip3 clostridium
28	71.5	8.8	268	1	IL1A_BOVIN	P08631 bos taurus
29	71.5	8.8	467	1	M3X8_HUMAN	P41279 homo sapien
30	71.5	8.8	527	1	RAG2_HUMAN	P55895 homo sapien
31	71	8.7	700	1	NONA_DROME	Q04047 drosophila
32	70.5	8.7	245	1	KDSB_FUSNN	Q8rf48 fuscobacteri
33	70.5	8.7	268	1	IL1A_CAPHI	P79161 capra hircu

RESULT 1

ID	IL18_HUMAN	STANDARD;	PRT;	193 AA.
AC	Q14116; O75599;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)			
DE	(IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).			
GN	IL18 OR IGIF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=96247646; PubMed=8666798;			
RA	Ushio S., Namba M., Okura T., Hattori K., Nakada Y., Akita K.,			
RA	Tanabe F., Konishi K., Micalef M., Fujii M., Torigoe K., Tanimoto T.,			
RA	Fukuda S., Ikeda M., Okamura H., Kurimoto M.;			
RT	"Cloning of the cDNA for human IFN-gamma-inducing factor, expression			
RT	in Escherichia coli, and studies on the biologic activities of the			
RT	protein.;"			
RL	J. Immunol. 156:4274-4279(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Yong D., Guixin D., Lihua H., Haitao W.;			
RT	"Cloning and sequencing of the cDNA for precursor hIL-18.;"			
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBSJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Liu J., Peng X., Yuan J., Qiang B.;			
RT	"Cloning of human interleukin 18 cDNA.;"			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Urinary bladder;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fabey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			

ALIGNMENTS

34	70.5	8.7	644	1	YGM4_YEAST	P53129 saccharomyc
35	70.5	8.7	659	1	DNAK_CHLAB	Q8gh79 chlamydomphi
36	70	8.6	198	1	VS11_ROTBA	P17467 rabbit rota
37	70	8.6	1647	1	SN24_HUMAN	P51532 homo sapien
38	70	8.6	2663	1	CENE_HUMAN	Q02224 homo sapien
39	70	8.6	4590	1	FATH_HUMAN	Q14517 homo sapien
40	69.5	8.6	268	1	IL1A_SHEEP	Q28579 ovis aries
41	69.5	8.6	351	1	RFL_TREPA	Q83090 treponema p
42	69.5	8.6	375	1	YVC5_CAEEL	Q18610 caenorhabdi
43	69.5	8.6	582	1	CRTI_CAPAN	P80093 capsaicum an
44	69.5	8.6	646	1	NOSZ_RALSO	Q8xob8 ralatonia s
45	69.5	8.6	919	1	RPO2_CAPVK	P16716 capripoxviz


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OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20012648; PubMed=10547157;
RX Shoda L.K., Zarlenga D.S., Hirano A., Brown W.C.;
RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity.";
RL J. Interferon Cytokine Res. 19:1169-1177(1999).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1
CC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF124789; AAF08686.1; -.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match 80.5%; Score 654; DB 1; Length 193;
Best Local Similarity 77.1%; Pred. No. 5,4e-54;
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDNDAPRTIFIISMYKDSQPRGM 60
Db 37 YFGKLEPKLSIIRNLNDQVLFINQGNQPVFEDMPDSCDNDAPRTIFIISMYKDSLTRGL 96

Qy 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKIDTKSDIIFQRSVPGHDKNQFESSY 120
Db 97 AVTISVQCKMSTLSCENKISFKEMNPPDNIDNEESDIIFQRSVPGHDKNQFESSLY 156

Qy 121 EGYFLACKERDLFKLILKKDELDGRSMTFTVQNEED 157
Db 157 KGFLACKENDLFLKILKKQDNRDKSVMTFTVQNGN 193

RESULT 4
IL18 PIG
ID IL18 PIG STANDARD; PRT; 192 AA.
AC O19073;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Foss D.L., Murtaugh M.P.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Penha-Goncalves M.N., Logan N.A., Nicolson L., Onions D.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

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RA Muneta Y., Mori Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=20260994; PubMed=10803849;
RA Fournout S., Dozois C.M., Yerie M., Pinton P., Fairbrother J.M.,
RA Oswald E., Oswald I.P.;
RT "Cloning, chromosomal location, and tissue expression of the gene for
RT pig interleukin-18.";
RL Immunogenetics 51:358-365(2000).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1
CC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
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CC -----
DR EMBL; U68701; AAC18415.1; -.
DR EMBL; Y11132; CAA72014.1; -.
DR EMBL; AB010003; BAA24135.1; -.
DR EMBL; AF191088; AAF71200.1; -.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005125; P:cytokine activity; IMP.
DR GO; GO:0001525; P:angiogenesis; ISS.
DR GO; GO:0042033; P:chemokine biosynthesis; ISS.
DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; IDA.
DR GO; GO:0042033; P:interferon-gamma biosynthesis; IDA.
DR GO; GO:0042035; P:positive regulation of activated T-cell pro. .; ISS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 35 BY SIMILARITY.
FT CHAIN 36 192 INTERLEUKIN-18.
SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 78.4%; Score 637; DB 1; Length 192;
Best Local Similarity 75.2%; Pred. No. 2e-52;
Matches 118; Conservative 24; Mismatches 15; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDNDAPRTIFIISMYKDSQPRGM 60
Db 36 YFGKLEPKLSIIRNLNDQVLFINQGNQPVFEDMPDSCDNDAPRTIFIISMYKDSLTRGL 95

Qy 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKIDTKSDIIFQRSVPGHDKNQFESSY 120
Db 96 AVTISVQCKMSTLSCENKISFKEMNPPDNIDNEESDIIFQRSVPGHDKNQFESSLY 155

Qy 121 EGYFLACKERDLFKLILKKDELDGRSMTFTVQNEED 157
Db 156 KGFLACKENDLFLKILKKQDNRDKSVMTFTVQNGN 192

RESULT 5
IL18 CANFA
ID IL18 CANFA STANDARD; PRT; 193 AA.
AC Q9XSR0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Canis familiaris (Dog).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=96115;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99309818; PubMed=10380699;
 RT Argyle D.J., McGillivray C., Nicolson L., Onions D.E.;
 RL "Cloning, sequencing, and characterization of dog interleukin-18.";
 CC Immunogenetics 49:541-543(1999).
 CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-1 family.
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 CC
 CC EMBL; Y11133; CAA72015.1; -;
 DR GO; GO:0005576; C:extracellular; TAS.
 DR GO; GO:0016506; F:apoptosis activator activity; IEP.
 DR GO; GO:0005125; F:cytokine activity; TAS.
 DR GO; GO:0005125; F:chemokine biosynthesis; ISS.
 DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; IEP.
 DR GO; GO:0042095; P:interferon-gamma biosynthesis; IDA.
 DR GO; GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.
 DR InterPro; IPR008996; Cytok_IL1_like.
 KW Cytokine.
 FT PROPEP 1 36 BY SIMILARITY.
 FT CHAIN 37 193 INTERLEUKIN-18.
 SQ SEQUENCE 193 AA; 22037 MW; 0D973E86F461F25 CRC64;
 Query Match 75.5%; Score 613; DB 1; Length 193;
 Best Local Similarity 73.7%; Pred. No. 3.5e-50;
 Matches 115; Conservative 23; Mismatches 18; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIIISMVKDSQPRGM 60
 DB 37 YFGKLEPKLSIRNLNDQVLFVNEGNQVFEVDEPDSCTDNAPRTIFIIISMVKDSLRLGL 96
 QY 61 AVTISVCKEKSIXLSCENKIIISFKEMNPPDNITKDYSDIIFQRSVPGHDKMKQFESSSY 120
 DB 97 AVTISVKYKWTSLCKNKTISFQKSPDPSINDRGNDIIFQRSVPGHDKIQFESSLY 156
 QY 121 EGYFLACERKDLFKLILKKEDELGDRSIMFTVQNE 156
 DB 157 KGHFLACKENDLFLKILKDKDENGDKSIMFTVQNK 192
 RESULT 6
 IL18_MOUSE
 ID IL18_MOUSE STANDARD; PRT; 192 AA.
 AC F70380;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
 DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
 GN IL18 OR IGIF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=96061009; PubMed=7477296;
 RA Okamura H., Tsutui H., Komatsu T., Yutsudo M., Hakura A.,

RA Tanimoto T., Torigoe K., Okura T., Nukada Y., Hattori K.
 RA Akita K., Namba M., Tanabe F., Konishi K., Fukuda S., Kurimoto M.;
 RT "Cloning of a new cytokine that induces IFN-gamma production by T
 RT cells.";
 RL Nature 378:88-91(1995).
 RN [2]
 RP SEQUENCE OF 1-191 FROM N.A.
 RC STRAIN=NOD; TISSUE=Pancreas;
 RX MEDLINE=97174346; PubMed=9022080;
 RA Rothe H., Jenkins N.A., Copeland N.G., Kolb H.;
 RT "Active stage of autoimmune diabetes is associated with the
 RT expression of a novel cytokine, IGIF, which is located near Idd2.";
 RL J. Clin. Invest. 99:469-474(1997).
 CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-1 family.
 CC
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 CC
 CC EMBL; D49949; BAA08705.1; -;
 DR EMBL; U66244; AAB49753.1; -;
 DR PIR; S60236; S60236.
 DR MGI; MGI:107936; IL18.
 DR GO; GO:0005576; C:extracellular; ISS.
 DR GO; GO:0016506; F:apoptosis activator activity; TAS.
 DR GO; GO:0005125; F:cytokine activity; ISS.
 DR GO; GO:0001525; P:angiogenesis; ISS.
 DR GO; GO:0042033; P:chemokine biosynthesis; ISS.
 DR GO; GO:0042253; P:granulocyte macrophage colony-stimulating f. .; ISS.
 DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; TAS.
 DR GO; GO:0042095; P:interferon-gamma biosynthesis; IMP.
 DR GO; GO:0042231; P:interleukin-13 biosynthesis; TAS.
 DR GO; GO:0042104; P:interleukin-2 biosynthesis; ISS.
 DR GO; GO:0030155; P:positive regulation of activated T-cell pro. .; ISS.
 DR GO; GO:0030431; P:sleep; ISS.
 DR InterPro; IPR008996; Cytok_IL1_like.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR SMART; SM00125; IL1; 1.
 KW Cytokine.
 FT PROPEP 1 35
 FT CHAIN 36 192 INTERLEUKIN-18.
 FT CONFLICT 183 185 MFT -> IS (IN REF. 2).
 SQ SEQUENCE 192 AA; 22135 MW; 8FED938473874D63 CRC64;
 Query Match 63.4%; Score 515; DB 1; Length 192;
 Best Local Similarity 64.9%; Pred. No. 4.7e-41;
 Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;
 QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIIISMVKDSQPRGMA 61
 DB 37 FGLRHCTAVIRNLNDQVLFVDK-RQPVFEDMTDIDQASFPQRLIIYMYKDSVRGLA 95
 QY 62 VTISVCKEKSIXLSCENKIIISFKEMNPPDNITKDYSDIIFQRSVPGHDKMKQFESSSY 121
 DB 96 VTLSVKDSKMSLTSLCKNKTISFEEMDPENDDIQSDLIFFQKRVPGH-NKMEFESSLY 154
 QY 122 GYFLACERKDLFKLILKKEDELGDRSIMFTVQNE 155
 DB 155 GHFLACQEDDAFLKILKDKDENGDKSVMTLTN 189
 RESULT 7
 IL18_RAT


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RESULT 9
FAT2 DROME
ID FAT2 DROME STANDARD; PRT: 4705 AA.
AC Q9VW71; Q95S51;
DC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Putative fat-like cadherin-related tumor suppressor homolog
DE precursor.
GN FAT2 OR CG7749.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Dou L.E., Downes M., Duran R., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J.J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleby J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kimios I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster."
RN [2]
RP REVISIONS.
EX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Battencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [3]
RP SEQUENCE OF 3837-4705 FROM N.A.

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RC STRAIN=Berkeley; TISSUE=Ovary;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Kronmiller B., Pacleby J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource."
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein (potential).
CC -!- SIMILARITY: Contains 34 cadherin domains.
CC -!- SIMILARITY: Contains 5 EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin G-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE003515; AAF49078.2; -
DR EMBL; AY060955; AAL28503.1; ALT_INIT.
DR EMBL; AY118666; AAM50035.1; ALT_INIT.
DR HSSP; P15116; INCI.
DR FlyBase; FBgn0036930; fat2.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0008014; P:calcium-dependent cell adhesion molecule ac. .; ISS.
DR GO; GO:0016339; P:calcium-dependent cell-cell adhesion; ISS.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR003985; ConA-like_lect_gl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001791; Laminin_G.
DR Pfam; PF000028; cadherin; 31.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF00054; laminin G; 1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00181; EGF; 6.
DR SMART; SM00282; LamG; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00232; CADHERIN_1; 18.
DR PROSITE; PS0268; CADHERIN_2; 34.
DR PROSITE; PS00022; EGF_1; 5.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 5.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 1.
KW Hypothetical protein; Cell adhesion; Signal; Glycoprotein;
KW Transmembrane; Calcium; Calcium-binding; Repeat; EGF-like domain.
FT SIGNAL 1 35
FT CHAIN 36 4705
FT PUTATIVE FAT-LIKE CADHERIN-RELATED TUMOR
FT SUPPRESSOR HOMOLOG.
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1648 1668
FT DOMAIN 1669 4705
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 60 180
FT CADHERIN 1.
FT DOMAIN 181 288
FT CADHERIN 2.
FT DOMAIN 285 397
FT CADHERIN 3.
FT DOMAIN 398 504
FT CADHERIN 4.
FT DOMAIN 505 610
FT CADHERIN 5.
FT DOMAIN 611 713
FT CADHERIN 6.
FT DOMAIN 770 874
FT CADHERIN 7.
FT DOMAIN 875 977
FT CADHERIN 8.
FT DOMAIN 978 1085
FT CADHERIN 9.
FT DOMAIN 1086 1195
FT CADHERIN 10.
FT DOMAIN 1191 1296
FT CADHERIN 11.
FT DOMAIN 1297 1402
FT CADHERIN 12.
FT DOMAIN 1405 1503
FT CADHERIN 13.
FT DOMAIN 1504 1609
FT CADHERIN 14.
FT DOMAIN 1610 1714
FT CADHERIN 15.

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FT DOMAIN 1715 1812 CADHERIN 16.
FT DOMAIN 1813 1929 CADHERIN 17.
FT DOMAIN 1930 2030 CADHERIN 18.
FT DOMAIN 2031 2137 CADHERIN 19.
FT DOMAIN 2138 2238 CADHERIN 20.
FT DOMAIN 2239 2338 CADHERIN 21.
FT DOMAIN 2339 2465 CADHERIN 22.
FT DOMAIN 2466 2567 CADHERIN 23.
FT DOMAIN 2568 2670 CADHERIN 24.
FT DOMAIN 2671 2779 CADHERIN 25.
FT DOMAIN 2780 2876 CADHERIN 26.
FT DOMAIN 2877 2983 CADHERIN 27.
FT DOMAIN 2984 3088 CADHERIN 28.
FT DOMAIN 3089 3185 CADHERIN 29.
FT DOMAIN 3186 3289 CADHERIN 30.
FT DOMAIN 3290 3394 CADHERIN 31.
FT DOMAIN 3395 3499 CADHERIN 32.
FT DOMAIN 3500 3604 CADHERIN 33.
FT DOMAIN 3605 3712 CADHERIN 34.
FT DOMAIN 3713 3819 EGF-LIKE 1.
FT DOMAIN 3820 3919 EGF-LIKE 2.
FT DOMAIN 3920 4019 LAMININ G-LIKE.
FT DOMAIN 4020 4129 EGF-LIKE 3.
FT DOMAIN 4130 4235 EGF-LIKE 4.
FT DOMAIN 4236 4342 EGF-LIKE 5.
FT DISULFID 3823 3835 POTENTIAL.
FT DISULFID 3836 3867 POTENTIAL.
FT DISULFID 3868 3878 POTENTIAL.
FT DISULFID 3879 3896 POTENTIAL.
FT DISULFID 3897 3907 POTENTIAL.
FT DISULFID 3908 3918 POTENTIAL.
FT DISULFID 4133 4144 POTENTIAL.
FT DISULFID 4145 4154 POTENTIAL.
FT DISULFID 4155 4165 POTENTIAL.
FT DISULFID 4166 4183 POTENTIAL.
FT DISULFID 4184 4193 POTENTIAL.
FT DISULFID 4194 4204 POTENTIAL.
FT DISULFID 4205 4258 POTENTIAL.
FT DISULFID 4259 4267 POTENTIAL.
FT DISULFID 4268 4278 POTENTIAL.
FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 779 779 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 843 843 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 923 923 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1106 1106 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1198 1198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1312 1312 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1439 1439 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1473 1473 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1511 1511 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 362 362 G -> E (IN REF. 3; AAL28503).
SQ SEQUENCE 4705 AA; 524564 MW; 6D387A489D2C33DE CRC64;

Query Match 10.8%; Score 88; DB 1; Length 4705;
Best Local Similarity 23.6%; Pred. No. 13;
Matches 38; Conservative 25; Mismatches 56; Indels 42; Gaps 7;

QY 32 DMTSDCDRNPRTTIFISMY-----KDSQPRGMATVISVKCKISXLSKCNKIISF--KE 85
DB 2124 DISVLVDVNDNCP--LFVNNPYVATVISIDDPKG---TIIMQVKAIDLSAENGVEVYELKK 2178
QY 86 MNPPDNIDKTSDDIIFQFQSVGHDKMOPFESSYEGYFLACEKERDL----- 133
DB 2179 NGNELFKLDRKSGBLSIKQHVGHNRNYELTVAAYDGAITPCSSAPLQVKVIDRMPVPF 2238
QY 134 ---FKLILKKED-----ELGDRSIMFTVQNE 156
DB 2239 EKQFTVSKVEDVMYSALSVSIEAESPLG-RSLIYITISSE 2278

RESULT 10
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IL1A_PIG
ID IL1A_PIG STANDARD; PRT; 270 AA.
AC P18430;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-1 alpha precursor (IL-1 alpha).
GN IL1A.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=903332454; PubMed=2377484;
RA Maliszewski C.R., Renshaw B.R., Schoenborn M.A., Urban J.F.,
RA Baker P.E.;
RT "Porcine IL-1 alpha cDNA nucleotide sequence.";
RL Nucleic Acids Res. 18:4282-4282(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA Huether M.J., Scamurra R.W., Murtaugh M.P., Molitor T.W.;
RL Submitted (XX-1992) to the EMBL/GenBank/DDJB databases.
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -!- SUBUNIT: Monomer.
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X52731; CAA36945.1; -.
CC EMBL; M86730; AAA73198.1; -.
CC PIR; I46620; I46620.
CC PIR; S10532; S10532.
CC HSSP; P01583; 11TA.
CC InterPro; IPR008996; Cytok_IL1_like.
CC InterPro; IPR003502; IL1_propep.
CC InterPro; IPR000975; Interleukin_1.
CC Pfam; PF00340; IL1; 1.
CC PIR; S10532; IL1; 1.
CC SMART; SM00125; IL1; 1.
CC PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 112
FT CHAIN 113 270 INTERLEUKIN-1 ALPHA.
FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 89 89 N -> I (IN REF. 2).
FT CONFLICT 242 242 F -> L (IN REF. 2).
FT CONFLICT 255 255 P -> R (IN REF. 2).
SQ SEQUENCE 270 AA; 5677BF2B0EF63839 CRC64;

Query Match 10.0%; Score 81.5; DB 1; Length 270;
Best Local Similarity 22.7%; Pred. No. 1.7;
Matches 30; Conservative 32; Mismatches 57; Indels 13; Gaps 6;
```

```

QY 8 KLSVIRNLNDVLFIDQGNRPLFEDMTD-----SDCRDNAPRTI-FIISMYKDSQPRGMAY 62
Db 123 KYNFMRVNHQICILNDRNQSIIRDPSQYLMAAVLNLDIAVDFDMAAYTSNDDSQLPV 182
QY 63 TISVKCEKISXLSCE--KIISFKEM-NPPDNIKDKTSIIFFORSVPGHDKMKQFESSS 119
Db 183 TLRIS-ETRLFSQAQNEDEPVLKLPETPKTKIDTSLLFFWEK-----HGMWYFKSA 237
QY 120 YEGYFLACEKER 131
Db 238 HPKLFIAATROEK 249

RESULT 11
IL1A RABIT
ID IL1A RABIT STANDARD; PRT; 267 AA.
AC P04822;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-1 alpha precursor (IL-1 alpha).
GN IL1A.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85297782; PubMed=2994016;
RA Fututani Y., Notsake M., Yamayoshi M., Yamagishi J., Nomura H.,
RA Ohue M., Furuta R., Fukui T., Yamada M., Nakamura S.;
RT "Cloning and characterization of the cDNAs for human and rabbit
interleukin-1 precursor."
RL Nucleic Acids Res. 13:5869-5882(1985).
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -!- SUBUNIT: Monomer.
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR HSSP; X02852; CAA26605.1; -.
DR IL1A; P01583; 1ITA.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR003502; IL1_pProep.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_pProep; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 112
FT CHAIN 113 267 INTERLEUKIN-1 ALPHA.
FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 267 AA; 30375 MW; 6D20533FD1FA4822 CRC64;

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Query Match 10.0%; Score 81; DB 1; Length 267;
Best Local Similarity 25.2%; Pred. No. 1.9;
Matches 32; Conservative 27; Mismatches 56; Indels 12; Gaps 5;

QY 12 IRNLNDVLFIDQGNRPLFEDMTDSDCRDNAPRTI-----FIISMYKDSQPRGMAYTISV 66
Db 127 LRIIKQFTLNDALNQSLVRDTSQYLRAPLQNLGDAVKFDMGVYMTSESDILPVTURI 186
QY 67 KCEKISXLSCE--KIISFKEM-NPPDNIKDKTSIIFFORSVPGHDKMKQFESSYEGY 123
Db 187 SQTPL-FVSAQNEDEPVLKEMPETPRIITDSBSILFFWET---QGNKNYFKSAANPOL 242
QY 124 FLACEKE 130
Db 243 FIATKPE 249

RESULT 12
DPO3_CLOPE
ID DPO3_CLOPE STANDARD; PRT; 1449 AA.
AC Q8XJR3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase III polc-type (EC 2.7.7.7) (polIII).
GN POLC OR CPE1691.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohehima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -!- FUNCTION: Required for replicative DNA synthesis. This DNA
CC polymerase also exhibits 3' to 5' exonuclease activity (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA} (N).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the DNA polymerase type-C family. Polc
CC subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP003191; BAB81397.1; -.
DR HAMAP; MF 00356; -.
DR InterPro; IPR006054; DnaQ.
DR InterPro; IPR006055; Exonuclease.
DR InterPro; IPR004013; PHP_C.
DR InterPro; IPR003141; PHP_N.
DR InterPro; IPR006308; Polc_gram_pos.
DR Pfam; PF00929; Exonuclease; 1.
DR Pfam; PF02811; PHP_C; 1.
DR Pfam; PF02231; PHP_N; 1.
DR SMART; SM00479; EXOIII; 1.
DR SMART; SM00481; POLIIIAC; 1.
DR TIGRFAMs; TIGR01405; polc_gram_pos; 1.
DR TIGRFAMs; TIGR01405; polc_gram_pos; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
Nuclease; Exonuclease; Complete proteome.

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FT DOMAIN 435 598 EXONUCLEASE.
SQ SEQUENCE 1449 AA; 163627 MW; AE24E2CE7D372B85 CRC64;

Query Match
Best Local Similarity 9.9%; Score 80; DB 1; Length 1449;
Matches 43; Conservative 21; Mismatches 52; Indels 42; Gaps 10;

QY 15 LNDQVLFIDQGNRPLFEDWTDSDC---RDNAPRTIFIISMYKDSQPRGMATVISVKCEKI 71
DQ 1196 LNAQVFIKEGYTTL-----KDCIATRDD---IMVLYMKDLPPK-TAFIMEKVRKG 1244
QY 72 SYLSCENKIISFENPDP-NIKDTSKDIIFQSRVPGHD-----NKQPFESS 118
DQ 1245 KGLSEDEAL-MREKNVDPWYTESCKRIKYMPPK---GHAVAYVMVAVRIAYKYVYPEA 1300
QY 119 SYEGVF-----LACEKERDLFLKLLKKEDELGD 146
DQ 1301 YTTVTFVTRADDFDADLICKGE-EAIIKAKWEELSLGN 1337

RESULT 13
DQAK CHLCV
ID DQAK CHLCV STANDARD; PRT; 664 AA.
AC Q824B2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Chapterone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70).
GN DQAK OR CCA00241.
OS Chlamydomophila caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83557;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22569155; PubMed=12682364;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T., Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A., Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O., Salberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavol P.M., Fraser C.M.;
RA "Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae.";
RL Nucleic Acids Res. 31:2134-2147(2003).
CC -!- FUNCTION: Acts as a chaperone (By similarity).
CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC
CC EMBL; AE016994; AAP04992.1; -.
CC TIGR; CCA00241; -.
CC HAMAP; MF_00332; -.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC ProDom; PD000089; Hsp70; 1.
CC PROSITE; PS00297; HSP70.1; 1.
CC PROSITE; PS00329; HSP70.2; 1.
CC PROSITE; PS01036; HSP70.3; 1.
CC Chapterone; ATP-binding; Heat shock; Phosphorylation; Complete proteome.
KW MOD_RES 201 201 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT SEQUENCE 664 AA; 71475 MW; 5C2F023B44984934 CRC64;

Query Match
Best Local Similarity 9.5%; Score 77.5; DB 1; Length 674;
Matches 30; Conservative 15; Mismatches 40; Indels 31; Gaps 5;

QY 17 DOVLFIDQGNRPLF-----DMTDSQR-----DNAPRTIFIISMYKDSQPRGMA 61
DQ 547 EDLYLYDE-NKEIFEKAGFKISDFGDSNIRIEVYFLDKLNPTELISMINLKKWGTG 605
QY 62 VTISVKCEKISLSC-----NKIISFKEM-----NPPDNIKOTKSDIIF 102
DQ 62 VTISVKCEKISLSC-----NKIISFKEM-----NPPDNIKOTKSDIIF 102

Query Match
Best Local Similarity 25.9%; Pred. No. 12;
Matches 30; Conservative 15; Mismatches 40; Indels 31; Gaps 5;

SQ SEQUENCE 674 AA; 77205 MW; 2380566BB4500A3D CRC64;

Query Match
Best Local Similarity 9.8%; Score 79.5; DB 1; Length 664;
Matches 26; Conservative 12; Mismatches 35; Indels 15; Gaps 3;

QY 36 SDCRDNAPRTIF-----IISMYKDSQPRGMATVISVKCEKISLSCENKIISFENPDPN 91
DQ 531 SDARNEADSMIFRAKAIKAIKAIKAIKAIKAIKAIKAIKAIKAIKAIKAIKAIKAIK 582
QY 92 IKDTSKDIIFQSRVPGHDNRKQPFESS 119
DQ 593 IKDASEEL---SRHMOKIGEAQSQSAS 607

RESULT 14
MUTL CLOPE
ID MUTL CLOPE STANDARD; PRT; 674 AA.
AC Q8XL66;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA mismatch repair protein mutL.
GN MUTL OR CPE1156.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RA "Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
RL CC
CC -!- FUNCTION: This protein is involved in the repair of mismatches in DNA. It is required for dam-dependent methyl-directed DNA mismatch repair. May act as a "molecular matchmaker", a protein that promotes the formation of a stable complex between two or more DNA-binding proteins in an ATP-dependent manner without itself being part of a final effector complex (By similarity).
CC -!- SIMILARITY: Belongs to the DNA mismatch repair mutL/hexB family.
CC
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CC
CC EMBL; AP003189; BAB80862.1; -.
CC HAMAP; MF_00149; -.
CC InterPro; IPR003594; ATPbind_ATPase.
CC InterPro; IPR002099; DNA_mis_repair.
CC Pfam; PF01119; DNA_mis_repair; 1.
CC Pfam; PF02518; HATPase_C; 1.
CC SMART; SM00387; HATPase_C; 1.
CC TIGRfam; TIGR00585; mutL; 1.
CC PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
CC DNA repair; Complete proteome.
KW DNA repair; Complete proteome.
SQ SEQUENCE 674 AA; 77205 MW; 2380566BB4500A3D CRC64;
```


Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	798	98.3	193	4	Q96KJ8	homo sapien
2	792	97.5	193	6	Q9BG15	macaca mula
3	654	80.5	178	6	Q9MZL8	bos taurus
4	648	79.8	193	6	Q9GL09	ovis aries
5	634	78.1	192	6	Q95M33	felis silve
6	633	78.0	192	6	Q865B8	felis silve
7	626	77.1	192	6	Q9N1P7	aus scrofa
8	536.5	66.1	195	11	Q80Y07	meriones un
9	515	63.4	189	11	Q80S58	mus musculus
10	441	54.3	196	11	Q91Z66	sigmodon hi
11	313	38.5	84	6	Q95LE7	canis famli
12	204	25.1	45	4	Q9NQ49	homo sapien
13	193	23.8	211	13	Q98SQ1	anas platyr
14	184.5	22.7	198	13	Q8AV26	meleagris g
15	182.5	22.5	198	13	Q918D2	gallus gall
16	86.5	10.7	376	11	Q8K487	mus musculus

```
Db 157 EGYFLTCERDLFKLILKKDELDGDRSIMFTVQNE 193
|||||
RESULT 2
Q9BG15 PRELIMINARY; PRT; 193 AA.
ID Q9BG15
AC Q9BG15
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin-18.
GN IL18.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21229850; PubMed=11331040;
RA Giavedoni L.D., Imhoof J.D., Farodi L.M., Velasquillo C.M.,
RA Hodara V.L.;
RT "Expression of the Interleukin-18 Gene from Rhesus Macaque by the
RT Simian Immunodeficiency Virus Does Not Result In Increased Viral
RT Replication.";
RL J. Interferon Cytokine Res. 21:173-180(2001).
DR EMBL; AF303732; AAK13416.1; -.
DR InterPro; IPR008996; Cytok IL1 like.
SQ SEQUENCE 193 AA; 22325 MW; B2BD29C03BB0B5E CRC64;

Query Match 97.5%; Score 792; DB 6; Length 193;
Best Local Similarity 95.5%; Pred. No. 1.1e-70;
Matches 150; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
|||||
Db 37 YFGKLESKLSIIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIINMYKDSQPRGM 96
|||||
Qy 61 AVTISVCKEISXLSKCNKIISFKEMNPPDNKDKTSIIFFQSRVPGHDNKMOPESSY 120
|||||
Db 97 AVAISVCKEISTLSKCNKIISFKEMNPPDNKDKTSIIFFQSRVPGHDNKMOPESSY 156
|||||
Qy 121 EGYFLACEKERDLFKLILKKDELDGDRSIMFTVQNE 157
|||||
Db 157 EGYFLACEKERDLFKLILKKDELDGDRSIMFTVQNE 193
|||||

RESULT 3
Q9MZL8 PRELIMINARY; PRT; 178 AA.
ID Q9MZL8
AC Q9MZL8
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin-18 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, Liver, and Blood;
RA Olsen S.C., Lee I.K., Mwangi S.M., Kehrli M., Bolin C.A.;
RT "Cloning of bovine interleukin-18, expression in Escherichia coli, and
RT characterization of the biologic activities of the recombinant
RT cytokine.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF173175; AAF89833.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; P:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
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DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
FT NON_TER 1
FT NON_TER 178
SQ SEQUENCE 178 AA; 20631 MW; 816D6B2B88ACB497 CRC64;

Query Match 80.5%; Score 654; DB 6; Length 178;
Best Local Similarity 77.1%; Pred. No. 4.9e-57;
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
|||||
Db 22 HFGKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIINMYKDSLTRGL 81
|||||
Qy 61 AVTISVCKEISXLSKCNKIISFKEMNPPDNKDKTSIIFFQSRVPGHDNKMOPESSY 120
|||||
Db 82 AVTISVCKEISXLSKCNKIISFKEMNPPDNKDKTSIIFFQSRVPGHDNKMOPESSY 141
|||||
Qy 121 EGYFLACEKERDLFKLILKKDELDGDRSIMFTVQNE 157
|||||
Db 142 KGYFLACKENDLFKLILKKQDDNRDKSVMTVQNK 178
|||||

RESULT 4
Q9GL09 PRELIMINARY; PRT; 193 AA.
ID Q9GL09
AC Q9GL09;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin-18 (IGIP).
GN IL-18.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Bailey S.L., Gossner A., Dalziel R., Hopkins J.;
RT "Cloning of Ovine Interleukin 18 cDNA.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ401033; CAC09326.2; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; P:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 193 AA; 22166 MW; CCD0A329062EF18C CRC64;

Query Match 79.8%; Score 648; DB 6; Length 193;
Best Local Similarity 77.7%; Pred. No. 2.1e-56;
Matches 122; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
|||||
Db 37 HFGKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIINMYKDSLTRGL 96
|||||
Qy 61 AVTISVCKEISXLSKCNKIISFKEMNPPDNKDKTSIIFFQSRVPGHDNKMOPESSY 120
|||||
Db 97 AVTISVCKEISXLSKCNKIISFKEMNPPDNKDKTSIIFFQSRVPGHDNKMOPESSY 156
|||||
Qy 121 EGYFLACEKERDLFKLILKKDELDGDRSIMFTVQNE 157
|||||
Db 157 KGYFLACKENDLFKLILKKQDDNRDKSVMTVQNK 193
|||||

RESULT 5
Q95M33 PRELIMINARY; PRT; 192 AA.
ID Q95M33
AC Q95M33;
```

Db 156 KGYPFLACEKEKDLFKLILKKDNGDKSIMFTVQNK 191

RESULT 7

Q9N1P7 PRELIMINARY; PRT; 192 AA.

ID Q9N1P7 PRELIMINARY; PRT; 192 AA.

AC Q9N1P7, 2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Interleukin-18.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OC NCBI_TaxID=9823;

OC [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Lung;

RC MEDLINE=20356335; PubMed=10901174;

RA Oem J.K., Song H.J., Kang S.W., Jeong W.S.;

RA "Cloning, sequencing, and expression of porcine interleukin-18 in

RT Escherichia coli.";

RL Mol. Cells 10:343-347(2000).

DR EMBL: AF176949; AAF35169.1; -

DR GO: GO:0005576; C:extracellular; IEA.

DR GO: GO:0005149; F:interleukin-1 receptor binding; IEA.

DR GO: GO:0006955; P:immune response; IEA.

DR InterPro: IPR008996; Cytok IL1 like.

DR InterPro: IPR000975; Interleukin_1.

DR SMART: SM00125; IL1; 1

DR SQ SEQUENCE 192 AA; 21969 MW; AS1EB7A4E221A16D CRC64;

Query Match 77.1%; Score 626; DB 6; Length 192;

Best Local Similarity 73.9%; Pred. No. 3.2e-54;

Matches 116; Conservative 25; Mismatches 16; Indels 0; Gaps 0

Qy 1 YFGKLESLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMVKDSQPRGM 60

Db 36 YFGKLEPLSIIRNLNDQVLFINQHQAVFEDMPDSCSDNAPQTVFIIMYKDSLTRL 95

Qy 61 AVTISVCKEKLXSLSCNKLIISFKEMPPDNIKDTKSDIIFQRSVPGHDKMKQFESSY 120

Db 96 AVTISVCKKMTSLSCNKTKLSFKEMPPDNIIDEGNDIIFQRSVPGHDDKIQFESSLY 155

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

Db 156 KGYPFLACEKENDLFKLILKEKDECGDKSITFTVQSKN 192

RESULT 8

Q80Y07 PRELIMINARY; PRT; 195 AA.

ID Q80Y07 PRELIMINARY; PRT; 195 AA.

AC Q80Y07, 2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Interleukin 18.

OS Irlu.

OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil),

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;

OC Meriones.

OC NCBI_TaxID=10047;

OC [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Peritoneum;

RC MEDLINE=22593022; PubMed=12706898;

RA Gaucher D., Chadee K.;

RA "Gerbil interleukin-18 and caspase-1: cloning, expression and

RT characterization."

RL Gene 307:159-166(2003).

DR EMBL: AY095932; AA034434.1; -

DR InterPro: IPR008996; Cytok IL1 like.

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SQ SEQUENCE 195 AA; 22172 MW; C6P8153117953154D CRC64;

Query Match 66.1%; Score 536.5; DB 11; Length 195;
Best Local Similarity 65.8%; Pred. No. 2.5e-45;
Matches 100; Conservative 29; Mismatches 22; Indels 1; Gaps 1;

QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGMA 61
DB 39 FGRLSSTAVIRNNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGMA 98
QY 62 VTISVKCEKISXLSCKENKIISFKENPPDNKDTSDIIFQFORSVPGHDKNQPFESSY 121
DB 99 VTLVKDTMTATLSCKENKIISFEENPPENIDDTESDLIFQKRVPGH-NKMQFESSLY 157

QY 122 GYFLACEKERDLFKLILKKEDELDGRSMTFTVN 153
DB 158 GHFLACQKEEDAFKILKKKDKDNGKSVNFTV 189

RESULT 9
Q80SS8 PRELIMINARY; PRT; 189 AA.
AC Q80SS8;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Interleukin 18.
GN IL18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.S/Dvte, and SJL/J; TISSUE=Spleen;
RA Gao J., Teuscher C.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY157834; AAC21309.1; -.
DR EMBL; AY157835; AAC21310.1; -.
DR InterPro; IPR008996; Cytok_IL1 like.
SQ SEQUENCE 189 AA; 21862 MW; E8P95EC01864665 CRC64;

Query Match 63.4%; Score 515; DB 11; Length 189;
Best Local Similarity 64.9%; Pred. No. 3.2e-43;
Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;

QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGMA 61
DB 34 FGRLHCTAVIRNNDQVLFVDK-RQPVFEDMTDIDQASSEFQTLIIYMYKDSVRGLA 92
QY 62 VTISVKCEKISXLSCKENKIISFKENPPDNKDTSDIIFQFORSVPGHDKNQPFESSY 121
DB 93 VTLSVKSKMSTLSCKENKIISFEENPPENIDDTESDLIFQKRVPGH-NKMQFESSLY 151

QY 122 GYFLACEKERDLFKLILKKEDELDGRSMTFTVN 155
DB 152 GHFLACQKEEDAFKILKKKDKDNGKSVNFTLN 185

RESULT 10
Q91Z66 PRELIMINARY; PRT; 196 AA.
AC Q91Z66;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Interleukin 18.
GN IL18.
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;

[1]
RN SEQUENCE FROM N.A.
RP Blanco J.C., Pletneva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY059406; AAL26703.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008996; Cytok_IL1 like.
DR InterPro; IPR00975; Interleukin_1.
DR SMART; SM00125; IL1_1.
SQ SEQUENCE 196 AA; 22345 MW; E27C5BDC397F951C CRC64;

Query Match 54.3%; Score 441; DB 11; Length 196;
Best Local Similarity 59.4%; Pred. No. 7.5e-36;
Matches 92; Conservative 24; Mismatches 37; Indels 2; Gaps 2;

QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 39 FFKESSTAVIRNNDQVLFIDREKSPVFEDMPDADQKANAQTRLIIMYKTFNPGGL 98
QY 61 AVTISVKCEKISXLSCKENKIISFKENPPDNKDTSDIIFQFORSVPGHDKNQPFESSY 120
DB 99 PVTLSVRDRTMTLSCKNQIISFEENPPLEIDGTGKSDLIFQRAVPGH-NKMQFESSLH 157
QY 121 EGYFLACEKERDLFKLILKKEDELDGRSMTFTVN 155
DB 158 EGHLACERDGSFKLILKKKDNWDTSIITFTVN 192

RESULT 11
Q95LE7 PRELIMINARY; PRT; 84 AA.
AC Q95LE7
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE IL-18 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Chamizo C., Rubio J.M., Moreno J., Alvar J.;
RT "Semi-quantification of canine cytokine expression by one tube RT-PCR.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF327900; AAL26920.1; -.
DR InterPro; IPR008996; Cytok_IL1 like.
FT NON_TER 1 84
FT TER 84 84
SQ SEQUENCE 84 AA; 9568 MW; 19BD9E27F336774B CRC64;

Query Match 38.5%; Score 313; DB 6; Length 84;
Best Local Similarity 74.7%; Pred. No. 1.5e-23;
Matches 59; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 5 YFGKLEPKLSIIRNLNDQVLFVNEGNQVFEDMPDSDCTDNAPRTIFIIMYKDSLTRGL 64
QY 61 AVTISVKCEKISXLSCKENK 79
DB 65 AVTISVKYKTMSTLSCKNK 83

RESULT 12
Q9NQ49 PRELIMINARY; PRT; 45 AA.
AC Q9NQ49
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DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin-18 (Fragment).
GN IL-18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fathan A.J., Pravica V., Hutchinson I.V.;
RT "Identification of Human Interleukin-18 gene polymorphisms.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295724; CAC01436.1; -.
DR InterPro; IPR008996; Cytok_IL1_like.
FT NON_TER 1
FT NON_TER 45
FT NON_TER 45
SQ SEQUENCE 45 AA; 5266 MW; DF3A626507B3D61A CRC64;

Query Match 25.1%; Score 204; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 4.7e-13;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTSDCR 39
DB 7 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTSDCR 45

RESULT 13
ID Q98SQ1 PRELIMINARY; PRT; 211 AA.
AC Q98SQ1;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin-18 (Fragment).
GN IL-18.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromia; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8939;
RN [1]
RP SEQUENCE FROM N.A.
RA Chan W.-S., Warr G.W., Middleton D.L., Lundquist M.L., Higgins D.A.;
RT "Anas platyrhynchos T-cell antigens, IL-18 gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF336122; AAK26322.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008996; Cytok_IL1_like.
DR SMART; SM00125; IL1; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 211 AA; 24541 MW; CA6FC63538211B2B CRC64;

Query Match 23.8%; Score 193; DB 13; Length 211;
Best Local Similarity 36.5%; Pred. No. 3.3e-11;
Matches 61; Conservative 29; Mismatches 63; Indels 14; Gaps 9;

QY 2 FGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMVKDSQP-RG 59
DB 43 FSKETLHRLFNVNSQLVVRPDLNMAAFEDVTDQEMKSGGMN-FCMHCYKTTTPSAG 101

QY 60 MAVTISVKCE-KISKLSCEK-IL-18 share high sequence
RL "cDNA cloning of biologically active chicken Interleukin-18.";
DR EMBL; AJ277865; CAB96214.1; -.
DR InterPro; IPR008996; Cytok_IL1_like.
FT CHAIN 30 198 INTERLEUKIN 18.
SQ SEQUENCE 198 AA; 22918 MW; 29BB77DC3E3C6600 CRC64;

Query Match 22.5%; Score 182.5; DB 13; Length 198;
Matches 58; Conservative 30; Mismatches 65; Indels 13; Gaps 7;

QY 2 FGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMVKDSQP-RG 59
DB 31 FCKETIKLFRNVNSQLVVRPDLNMAAFEDVTDQEVKSGS-GMYFIHCYKTTTPSAG 89

QY 60 MAVTISVKCEKISKLSCEK-IL-18 share high sequence
DB 90 MPVAFSVQVEDKSYVMCEEHGKMWVFRGEVPEKDPG-ESNMIFPKKTTSCSKAF 148

QY 114 QFESSYEGYFLACEKRDLPKILKK-IL-18 share high sequence
DB 149 KFEYSLERGMFLAFEEEDSLRKLILKKLPREDEVDETTKFTVTSRNE 194

RESULT 15
ID Q918D2 PRELIMINARY; PRT; 198 AA.
AC Q918D2;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin 18.
GN IL-18.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromia; Aves; Neognathae; Galliformes; Phasianinae;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20508574; PubMed=11054275;
RA Schneider K., Puehler E., Baeuerle D., Elvers S., Staeheli P.,
RA Kasper B., Weining K.C.;
RT "cDNA cloning of biologically active chicken Interleukin-18.";
RL J. Interferon Cytokine Res. 20:879-883(2000).
DR EMBL; AJ277865; CAB96214.1; -.
DR InterPro; IPR008996; Cytok_IL1_like.
FT CHAIN 30 198 INTERLEUKIN 18.
SQ SEQUENCE 198 AA; 22918 MW; 29BB77DC3E3C6600 CRC64;

Query Match 22.5%; Score 182.5; DB 13; Length 198;
Matches 58; Conservative 30; Mismatches 65; Indels 13; Gaps 7;

QY 2 FGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMVKDSQP-RG 59
DB 31 FCKETIKLFRNVNSQLVVRPDLNMAAFEDVTDQEVKSGS-GMYFIHCYKTTTPSAG 89

QY 60 MAVTISVKCEKISKLSCEK-IL-18 share high sequence
DB 90 MPVAFSVQVEDKSYVMCEEHGKMWVFRGEVPEKDPG-ESNMIFPKKTTSCSKAF 148

QY 114 QFESSYEGYFLACEKRDLPKILKK-IL-18 share high sequence
DB 149 KFEYSLERGMFLAFEEEDSLRKLILKKLPREDEVDETTKFTVTSRNE 194
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OM protein - protein search, using sw model

Run on: August 19, 2004, 13:34:05 ; Search time 19 Seconds
(without alignments)

426.594 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	157	4	US-08-982-285-4
2	811	99.9	157	4	US-09-700-609-1
3	811	99.9	158	4	US-09-398-412B-7
4	810	99.8	157	2	US-08-896-605A-6
5	810	99.8	157	2	US-08-896-501A-4
6	810	99.8	157	3	US-08-884-324-1
7	810	99.8	157	3	US-08-996-338-26
8	810	99.8	157	3	US-08-558-818-1
9	810	99.8	157	3	US-08-974-469A-1
10	810	99.8	157	3	US-08-832-180-1
11	810	99.8	157	3	US-08-832-198-6
12	810	99.8	157	4	US-09-819-902-6
13	810	99.8	157	4	US-09-752-510-6
14	810	99.8	157	4	US-09-711-899-1
15	810	99.8	157	4	US-09-556-972-26
16	810	99.8	157	4	US-09-649-063-1
17	810	99.8	193	2	US-08-896-605A-2
18	810	99.8	193	2	US-08-832-180-9
19	810	99.8	157	3	US-08-832-180-6
20	801	98.6	157	4	US-08-982-285-6
21	792	97.5	193	4	US-09-597-576-2
22	791	97.4	157	4	US-08-982-285-7
23	791	97.4	157	4	US-08-982-285-8
24	782	96.3	157	4	US-08-982-285-11
25	781	96.2	157	4	US-08-982-285-9
26	772	95.1	157	4	US-08-982-285-12
27	771	95.0	157	4	US-08-982-285-10

28 613 75.5 179 4 US-09-445-724B-14 Sequence 14, Appl
29 613 75.5 193 4 US-09-445-724B-2 Sequence 2, Appl
30 613 75.5 193 4 US-09-445-724B-6 Sequence 6, Appl
31 517 63.7 157 4 US-08-982-285-13 Sequence 13, Appl
32 515 63.4 157 4 US-08-982-285-5 Sequence 5, Appl
33 515 63.4 157 4 US-09-700-609-2 Sequence 2, Appl
34 515 63.4 158 4 US-09-398-412B-8 Sequence 8, Appl
35 513 63.2 157 2 US-08-502-535B-2 Sequence 2, Appl
36 513 63.2 157 2 US-08-908-005A-2 Sequence 2, Appl
37 513 63.2 157 3 US-08-996-338-27 Sequence 27, Appl
38 513 63.2 157 3 US-08-558-818-7 Sequence 7, Appl
39 513 63.2 157 3 US-08-974-469A-7 Sequence 7, Appl
40 513 63.2 157 3 US-08-832-180-8 Sequence 8, Appl
41 513 63.2 157 3 US-08-832-198-11 Sequence 11, Appl
42 513 63.2 157 3 US-09-253-523-2 Sequence 2, Appl
43 513 63.2 157 3 US-09-251-911-2 Sequence 2, Appl
44 513 63.2 157 4 US-09-819-902-11 Sequence 11, Appl
45 513 63.2 157 4 US-09-752-510-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-982-285-4
; Sequence 4, Application US/08982285
; Patent No. 6476197
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Koza
; APPLICANT: OKAMOTO, Iwao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 7th Street N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/982,285
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 333,037/96
; FILING DATE: No. 6476197ember 29, 1996
; APPLICATION NUMBER: JP 20,906/97
; FILING DATE: January 21, 1997
; APPLICATION NUMBER: JP 10,053,503
; FILING DATE: No. 6476197ember 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: YAMAMOTO=15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-982-285-4

Query Match 99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.8e-88;
Matches 156; Conservative 1; Indels 0; Gaps 0;

Qy	1	YFGKLESLSVIRNLNDQVLFI	DQGNRPLF	EDMTDSDCRNAPRTFI	IISMYKDSQPRGM	60
Db	1	YFGKLESLSVIRNLNDQVLFI	DQGNRPLF	EDMTDSDCRNAPRTFI	IISMYKDSQPRGM	60
Qy	61	AVTISVKEKISLSCENKLI	SFKEMNPPDNI	KOTKSDIIF	FORSPVGHDKNKQFESSY	120
Db	61	AVTISVKEKISTLSCENKLI	SFKEMNPPDNI	KOTKSDIIF	FORSPVGHDKNKQFESSY	120
Qy	121	EGYFLACEKERDLFLKIL	IKGEDELGDRS	IMFTVQNE	157	
Db	121	EGYFLACEKERDLFLKIL	IKGEDELGDRS	IMFTVQNE	157	

RESULT 2

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US-09-700-609-1
; Sequence 1, Application US/09700609
; Patent No. 6582689
; GENERAL INFORMATION:
; APPLICANT: Johnson, Randall K
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: P50777
; CURRENT APPLICATION NUMBER: US/09/700,609
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/086,560
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Human
US-09-700-609-1

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Query Match	99.9%	Score 811;	DB 4;	Length 157;
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Matches 156;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	YFGKLESKLSVIRNLNDQVLFDIDGNRPLFPEDMTDSDCRDNAPRTIFIISMYKDSQPSGM	60	
Db	1	YFGKLESKLSVIRNLNDQVLFDIDGNRPLFPEDMTDSDCRDNAPRTIFIISMYKDSQPSGM	60	
Qy	61	AVTISVCKEKISLSCENKIIISFKEMPPDNIKOTKSDIIIFQRSVPGHDKNQPFESSY	120	
Db	61	AVTISVCKEKISTLSCENKIIISFKEMPPDNIKOTKSDIIIFQRSVPGHDKNQPFESSY	120	
Qy	121	EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE	157	
Db	121	EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE	157	

RESULT 3

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US-09-398-412B-7
; Sequence 7, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage
; TITLE OF INVENTION: methods
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-398-412B-7
Query Match          99.9%   Score 811;   DB 4;   Length 158;

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Best Local Similarity 99.4%; Pred. No. 3.8e-88;	
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 YFGKLSKLSVIRNLNDQVLFDIQGNRPLFEDMTDSDCRDNAPRTIIISMYKDSQPRGM 60
Db	2 YFGKLSKLSVIRNLNDQVLFDIQGNRPLFEDMTDSDCRDNAPRTIIISMYKDSQPRGM 61
Qy	61 AVTISVKCEKISLSCENKIISPKEMPPNNIKDTKSDIIFQBSVPGHDNMQPFESSY 120
Db	62 AVTISVKCEKISTLSCENKIISPKEMPPNNIKDTKSDIIFQBSVPGHDNMQPFESSY 121
Qy	121 EGYFLACEKERDIFKLILKKEDELGDRSINFTQVNE 157
Db	122 EGYFLACEKERDIFKLILKKEDELGDRSINFTQVNE 158

RESULT 4

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US-08-896-605A-6
; Sequence 6, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,605A
; FILING DATE: 18 July 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207,691/1996
; FILING DATE: 19-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 156,062/1997
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-896-605A-6

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	Query Match	99.8%	Score 810	DB 2	Length 157
	Best Local Similarity	100.0%	Prod. No. 4.9e-88		
	Matches 157	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	YFGKLSKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIIISMYKDSQPRGM	60		
Db	1	YFGKLSKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIIISMYKDSQPRGM	60		
Qy	61	AVTISVKCEKISXLSCENKIIISFKEMPPNNIKDTKSDIIFFORSVFGHDNKMOFESSY	120		
Db	61	AVTISVKCEKISXLSCENKIIISFKEMPPNNIKDTKSDIIFFORSVFGHDNKMOFESSY	120		

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 5

US-08-896-501A-4

; Sequence 4, Application US/08896501A
; Patent No. 5891663

GENERAL INFORMATION:

; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/896,501A

FILING DATE: 18-JUL-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 213,267/1996

FILING DATE: 25-JUL-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 31,474/1997

FILING DATE: 31-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: TANIMOTO=3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 157 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-896-501A-4

Query Match 99.8%; Score 810; DB 2; Length 157;

Best Local Similarity 100.0%; Pred. No. 4.9e-88;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIIISMTYKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIIISMTYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPVGHDKMQFESSY 120

Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPVGHDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 6

US-08-884-324-1

; Sequence 1, Application US/08884324

; Patent No. 6060283

GENERAL INFORMATION:

; APPLICANT: Takanori OKURA
; APPLICANT: Kakuji TORIGOE
; APPLICANT: Masahi KURIMOTO
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
; TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,324
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 185,305/96
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKURA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-884-324-1

Query Match

Best Local Similarity 99.8%; Score 810; DB 3; Length 157;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIIISMTYKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIIISMTYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPVGHDKMQFESSY 120

Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPVGHDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 7

US-08-996-338-26

; Sequence 26, Application US/08996338

; Patent No. 6087116

GENERAL INFORMATION:

; APPLICANT: TORIGOE, Kakuji
; APPLICANT: OKURA, Takanori
; APPLICANT: KURIMOTO, Masahi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.

```
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,338
; FILING DATE: 22-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 74,697/1997
; FILING DATE: 12-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 215,488/1997
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 291,837/1997
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-996-338-26

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVCKEKISLSCENKIISFKEMNPPDNIKDKTSDIIFQRSVPGHDNKNQFESSY 120
DB 61 AVTISVCKEKISLSCENKIISFKEMNPPDNIKDKTSDIIFQRSVPGHDNKNQFESSY 120
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 8
US-08-558-818-1
; Sequence 1, Application US/08558818
; Patent No. 6197297
; GENERAL INFORMATION:
; APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUJO
; APPLICANT: TORIGOE, Toshio
; APPLICANT: KUNIKATA, Toshiro
; APPLICANT: TANIGUCHI, Mutsuko
; APPLICANT: KOHNO, Keizo
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: FELICI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/558,818
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: JP 58,240/95
; PRIOR APPLICATION DATA: February 23, 1995
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-558-818-1

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVCKEKISLSCENKIISFKEMNPPDNIKDKTSDIIFQRSVPGHDNKNQFESSY 120
DB 61 AVTISVCKEKISLSCENKIISFKEMNPPDNIKDKTSDIIFQRSVPGHDNKNQFESSY 120
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 9
US-08-974-469A-1
; Sequence 1, Application US/08974469A
; Patent No. 6207641
; GENERAL INFORMATION:
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUJO
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: FUKUDA, Shigeharu
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,469A
; FILING DATE:
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,879
; FILING DATE:
; APPLICATION NUMBER: JP 78,357/95
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: JP 274,988/95
; FILING DATE: September 29, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOB=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-974-469A-1

Query Match          99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIDKTKSDIIFQORSVPGHNDKMQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIDKTKSDIIFQORSVPGHNDKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 10
US-08-832-180-1
; Sequence 1, Application US/08832180
; Patent No. 6214584
; GENERAL INFORMATION:
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUJO
; APPLICANT: USHIO, Shimpei
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: OKAMURA, Haruki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,180
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/558,191
; FILING DATE:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 96-067434
; FILING DATE:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 96-067434
; FILING DATE:

; APPLICATION NUMBER: JP 304,203/94
; FILING DATE: No. 6214584ember 15, 1994
; APPLICATION NUMBER: 10048102
; FILING DATE: September 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: USHIO=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-832-180-1

Query Match          99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIDKTKSDIIFQORSVPGHNDKMQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIDKTKSDIIFQORSVPGHNDKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 11
US-08-832-198-6
; Sequence 6, Application US/08832198
; Patent No. 6242255
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; APPLICANT: NUKADA, Yoshiyuki
; APPLICANT: FUJII, Mitsukiyo
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSES: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,198
; FILING DATE: 08-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 96-067434
; FILING DATE:

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;
; FILING DATE: 29-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; 'ile' or 'Thr'
; US-08-832-198-6

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSNENKIISFKEMNPPDNKDTKSDIIFQRSVPGHDNKKMFESSY 120
Db 61 AVTISVKCEKISXLSNENKIISFKEMNPPDNKDTKSDIIFQRSVPGHDNKKMFESSY 120
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157

RESULT 12
US-09-819-902-6
; Sequence 6, Application US/09819902
; Patent No. 6403079
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; NUKADA, Yoshiyuki
; FUJII, Mitsukiyo
; TANIMOTO, Tadao
; KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; PRODUCTION BY IMMUNOCOMPETENT CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/819,902
; FILING DATE: 29-Mar-2001
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/832,798
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725

;
; FILING DATE: 26-SEP-1995
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; 'ile' or 'Thr'
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
; US-09-819-902-6

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSNENKIISFKEMNPPDNKDTKSDIIFQRSVPGHDNKKMFESSY 120
Db 61 AVTISVKCEKISXLSNENKIISFKEMNPPDNKDTKSDIIFQRSVPGHDNKKMFESSY 120
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157

RESULT 13
US-09-752-510-6
; Sequence 6, Application US/09752510
; Patent No. 6441138
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; NUKADA, Yoshiyuki
; FUJII, Mitsukiyo
; TANIMOTO, Tadao
; KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; PRODUCTION BY IMMUNOCOMPETENT CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/752,510
; FILING DATE: 03-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: <Unknown>

APPLICATION NUMBER: JP 96-067434
FILING DATE: 29-FEB-1996
APPLICATION NUMBER: JP not yet received
FILING DATE: 20-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: AKITA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: "Xaa" in position 73 is either
'ile' or 'Thr'
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-752-510-6

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPDLFEDMTSDCDRNPARTFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPDLFEDMTSDCDRNPARTFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSDIIFQRSVPGHDKMQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSDIIFQRSVPGHDKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGRSIMFTVQNEED 157

RESULT 14
US-09-711-899-1
Sequence 1, Application US/09711899
Patent No. 6509449
GENERAL INFORMATION:
APPLICANT: <Unknown>
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
WHICH INDUCES INTERFERON- PRODUCTION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,899
FILING DATE: 13-NOV-2000
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/588,818
FILING DATE: 2000-11-15
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICI=1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-711-899-1

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPDLFEDMTSDCDRNPARTFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPDLFEDMTSDCDRNPARTFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSDIIFQRSVPGHDKMQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSDIIFQRSVPGHDKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGRSIMFTVQNEED 157

RESULT 15
US-09-556-972-26
Sequence 26, Application US/09556972
Patent No. 6559298
GENERAL INFORMATION:
APPLICANT: TORIGOE, Kakuji
OKURA, Takanori
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/556,972
FILING DATE: 24-Apr-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE=3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 157

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-556-972-26

Query Match      99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKMQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKMQFESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEQ 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEQ 157

Search completed: August 19, 2004, 13:37:15
Job time : 20 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 19, 2004, 13:35:10 ; Search time 46 Seconds
(without alignments)
1072.566 Million cell updates/sec

Title: US-09-716-356A-6
Perfect score: 812
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKDELGDRSIMFTVQNEED 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 314255058 residues

Total number of hits satisfying chosen parameters: 1295152

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	811	99.9	157	9	US-09-775-046-9	Sequence 9, Appli
2	811	99.9	157	10	US-09-030-061-6	Sequence 6, Appli
3	811	99.9	157	12	US-10-247-703-65	Sequence 65, Appl
4	811	99.9	157	12	US-10-247-703-71	Sequence 71, Appl
5	811	99.9	157	13	US-10-100-057-6	Sequence 6, Appli
6	811	99.9	157	13	US-10-094-153-2	Sequence 2, Appli
7	811	99.9	157	14	US-10-260-576-4	Sequence 4, Appli
8	811	99.9	157	14	US-10-297-136-1	Sequence 1, Appli
9	811	99.9	157	14	US-10-311-491-3	Sequence 3, Appli
10	811	99.9	157	15	US-10-397-786A-3	Sequence 3, Appli
11	811	99.9	157	16	US-10-280-609-1	Sequence 1, Appli
12	811	99.9	157	16	US-10-646-308-14	Sequence 14, Appli
13	811	99.9	157	16	US-10-695-195-7	Sequence 7, Appli
14	811	99.9	158	16	US-10-694-978-7	Sequence 7, Appli
15	811	99.9	177	12	US-10-247-703-69	Sequence 69, Appli

16	811	99.9	193	9	US-09-798-075-1	Sequence 1, Appli
17	811	99.9	193	9	US-09-770-528-8	Sequence 8, Appli
18	811	99.9	193	14	US-10-311-491-1	Sequence 1, Appli
19	811	99.9	193	16	US-10-679-201-5	Sequence 5, Appli
20	811	99.9	233	14	US-10-311-491-10	Sequence 10, Appli
21	810	99.8	157	8	US-08-996-140-1	Sequence 1, Appli
22	810	99.8	157	9	US-09-924-099-21	Sequence 21, Appli
23	810	99.8	157	14	US-10-327-069-1	Sequence 1, Appli
24	810	99.8	157	14	US-10-349-023-26	Sequence 26, Appli
25	810	99.8	193	16	US-10-646-308-13	Sequence 13, Appli
26	807	99.4	157	13	US-10-094-153-10	Sequence 10, Appli
27	807	99.4	193	13	US-10-094-153-9	Sequence 9, Appli
28	805	99.1	157	13	US-10-094-153-6	Sequence 6, Appli
29	805	99.1	157	13	US-10-094-153-7	Sequence 7, Appli
30	805	99.1	193	13	US-10-094-153-3	Sequence 3, Appli
31	805	99.1	193	13	US-10-094-153-4	Sequence 4, Appli
32	803	98.9	157	14	US-10-105-080-10	Sequence 10, Appli
33	803	98.9	193	14	US-10-105-080-4	Sequence 4, Appli
34	801	98.6	157	10	US-09-030-061-20	Sequence 20, Appli
35	801	98.6	157	13	US-10-100-057-20	Sequence 20, Appli
36	801	98.6	157	14	US-10-260-576-6	Sequence 6, Appli
37	799	98.4	157	12	US-10-247-703-77	Sequence 77, Appli
38	799	98.4	157	13	US-10-094-153-8	Sequence 8, Appli
39	799	98.4	193	13	US-10-094-153-5	Sequence 5, Appli
40	798	98.3	157	12	US-10-247-703-72	Sequence 72, Appli
41	795.5	98.0	156	15	US-10-414-774-1	Sequence 1, Appli
42	795	97.9	157	12	US-10-247-703-74	Sequence 74, Appli
43	792	97.5	157	12	US-10-247-703-75	Sequence 75, Appli
44	791	97.4	157	10	US-09-030-061-21	Sequence 21, Appli
45	791	97.4	157	10	US-09-030-061-22	Sequence 22, Appli

ALIGNMENTS

RESULT 1
US-09-775-046-9
; Sequence 9, Application US/09775046
; Patent No. US20020102234A1
; GENERAL INFORMATION:
; APPLICANT: Debets, Johannes Eduard Maria Antonius
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01073K
; CURRENT APPLICATION NUMBER: US/09/775,046
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/179,638
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-046-9

Query Match	99.9%	Score 811;	DB 9;	Length 157;
Best Local Similarity	99.4%	Pred. No. 3.1e-81;		
Matches 156;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
Qy	1	YFGKLESKLSVIRNLNDQVLFDQGNRPLFEDMTDSDCRDNAPRTIFIIISMTKDSQPRGM 60		
Db	1	YFGKLESKLSVIRNLNDQVLFDQGNRPLFEDMTDSDCRDNAPRTIFIIISMTKDSQPRGM 60		
Qy	61	AVTISVKCEKISLSCENKIIISFKEMNPPDNIKDTKSDIIFFQRSVPVGHDKMKQFESSY 120		
Db	61	AVTISVKCEKISLSCENKIIISFKEMNPPDNIKDTKSDIIFFQRSVPVGHDKMKQFESSY 120		
Qy	121	EGYFLACKEKRDLFKLIKKGDELGDRSIMFTVQNEED 157		
Db	121	EGYFLACKEKRDLFKLIKKGDELGDRSIMFTVQNEED 157		

RESULT 2

US-09-030-061-6
; Sequence 6, Application US/09030061
; Publication No. US20030095946A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; APPLICANT: HORWOOD, Nicole Joy
; APPLICANT: UDAGAWA, No. US20030095946A1uyuki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-030-061-6

Query Match 99.9%; Score 811; DB 10; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKQPESSSY 120
Db 61 AVTISVKEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKQPESSSY 120

Qy 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 3

US-10-247-703-65
; Sequence 65, Application US/10247703
; Publication No. US20030063597A1
; GENERAL INFORMATION:
; APPLICANT: Branigan, Patrick
; APPLICANT: Goletz, Theresa J
; APPLICANT: Knight, David M
; APPLICANT: McCarthy, Stephen G
; APPLICANT: Scallion, Bernard J

; APPLICANT: Snyder, Linda A
; TITLE OF INVENTION: NUCLEIC ACID VACCINES USING TUMOR ANTIGEN ENCODING NUCLEIC ACIDS
; FILE REFERENCE: CEN310
; CURRENT APPLICATION NUMBER: US/10/247,703
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 65
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-247-703-65

Query Match 99.9%; Score 811; DB 12; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKQPESSSY 120
Db 61 AVTISVKEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKQPESSSY 120

Qy 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 4

US-10-247-703-71
; Sequence 71, Application US/10247703
; Publication No. US20030063597A1
; GENERAL INFORMATION:
; APPLICANT: Branigan, Patrick
; APPLICANT: Goletz, Theresa J
; APPLICANT: Knight, David M
; APPLICANT: McCarthy, Stephen G
; APPLICANT: Scallion, Bernard J
; APPLICANT: Snyder, Linda A
; TITLE OF INVENTION: NUCLEIC ACID VACCINES USING TUMOR ANTIGEN ENCODING NUCLEIC ACIDS
; FILE REFERENCE: CEN310
; CURRENT APPLICATION NUMBER: US/10/247,703
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 71
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-247-703-71

Query Match 99.9%; Score 811; DB 12; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKQPESSSY 120
Db 61 AVTISVKEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKQPESSSY 120

Qy 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157


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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 157 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-260-576-4

Query Match      99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIKDKTSDIIFQRSVPVGHDKMKQFESSY 120
DB 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIKDKTSDIIFQRSVPVGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 8
US-10-297-136-1
; Sequence 1, Application US/10297136
; Publication No. US20030113292A1
; GENERAL INFORMATION:
; APPLICANT: ESSER, KLAUS M.
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: TAL-SINGER, RUTH
; APPLICANT: WOODNUTT, GARY
; APPLICANT: CHISARI, FRANCIS V.
; APPLICANT: DILLON, SUSAN B.
; TITLE OF INVENTION: Methods of Treating Viral Diseases with
; TITLE OF INVENTION: IL-18 and IL-18 Combinations
; FILE REFERENCE: P51144
; CURRENT APPLICATION NUMBER: US/10/297,136
; PRIOR FILING DATE: 2002-10-02
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/208,869
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-297-136-1

Query Match      99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIKDKTSDIIFQRSVPVGHDKMKQFESSY 120
DB 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIKDKTSDIIFQRSVPVGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 9
US-10-311-491-3
; Sequence 3, Application US/10311491
; Publication No. US20030143198A1
; GENERAL INFORMATION:
; APPLICANT: Johanson, Kyung O.
; APPLICANT: Kirkpatrick, Robert B.
; APPLICANT: Shatzman, Allan R.
; APPLICANT: Ho, Yen Sen
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Method for Preparing a Physiologically
; TITLE OF INVENTION: Active IL-18 Polypeptide
; FILE REFERENCE: P51137
; CURRENT APPLICATION NUMBER: US/10/311,491
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/18804
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/211,832
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/224,128
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/264,923
; PRIOR FILING DATE: 2001-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-311-491-3

Query Match      99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIKDKTSDIIFQRSVPVGHDKMKQFESSY 120
DB 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIKDKTSDIIFQRSVPVGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 10
US-10-397-786A-3
; Sequence 3, Application US/10397786A
; Publication No. US20040018195A1
; GENERAL INFORMATION:
; APPLICANT: Griswold, Donald
; APPLICANT: Li, Li
; APPLICANT: Li, Jian
; TITLE OF INVENTION: DIABETES DISEASE DERIVED PROTEINS, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN-0287
; CURRENT APPLICATION NUMBER: US/10/397,786A
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/367,902
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver 2.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-397-786A-3

Query Match      99.9%; Score 811; DB 15; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
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Db 1 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDKTSDIIFQSVPGHDNKKMQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDKTSDIIFQSVPGHDNKKMQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 11

US-10-280-609-1
; Sequence 1, Application US/10280609
; Publication No. US20040023336A1
; GENERAL INFORMATION:
; APPLICANT: Heavner, George
; APPLICANT: Snyder, Linda Anne
; APPLICANT: McCarthy, Stephen G.
; TITLE OF INVENTION: IL-18 OR MUT-IL-18R PROTEINS, ANTIBODIES, COMPOSITIONS,
; TITLE OF INVENTION: METHODS AND USES
; FILE REFERENCE: CEN0321
; CURRENT APPLICATION NUMBER: US/10/280,609
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/335,880
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-280-609-1

Query Match 99.9%; Score 811; DB 16; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Qy 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDKTSDIIFQSVPGHDNKKMQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDKTSDIIFQSVPGHDNKKMQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 12

US-10-646-308-14
; Sequence 14, Application US/10646308
; Publication No. US20040136992A1
; GENERAL INFORMATION:
; APPLICANT: BURTON, Paul B. J.
; APPLICANT: DEISHER, Theresa A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE
; FILE REFERENCE: 3432-B
; CURRENT APPLICATION NUMBER: US/10/646,308
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: --to be assigned--
; PRIOR FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: 60/406,418
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-646-308-14

Query Match 99.9%; Score 811; DB 16; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Qy 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDKTSDIIFQSVPGHDNKKMQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDKTSDIIFQSVPGHDNKKMQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 13

US-10-695-195-7
; Sequence 7, Application US/10695195
; Publication No. US20040068099A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/695,195
; FILING DATE: 27-Oct-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/398,412
; FILING DATE: 17-Sep-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0904K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-695-195-7

Query Match 99.9%; Score 811; DB 12; Length 158;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 2 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 61
Qy 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDKTSDIIFQSVPGHDNKKMQFESSY 120

Db 62 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIKOTKSDIIFFQRSVPGHDNKMQPESSSY 121
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 122 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 158

RESULT 14

US-10-694-978-7
; Sequence 7, Application US/10694978
; Publication No. US20040087766A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 27-Oct-2003
; APPLICATION NUMBER: US/10/694,978
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/398,412
; FILING DATE: 17-Sep-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0904K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-694-978-7

Query Match 99.9%; Score 811; DB 16; Length 158;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 2 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 61
Qy 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFFQRSVPGHDNKMQPESSSY 120
Db 62 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIKOTKSDIIFFQRSVPGHDNKMQPESSSY 121
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 122 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 158

RESULT 15

US-10-247-703-69
; Sequence 69, Application US/10247703
; Publication No. US20030063597A1
; GENERAL INFORMATION:

; APPLICANT: Branigan, Patrick
; APPLICANT: Goletz, Theresa J
; APPLICANT: Knight, David M
; APPLICANT: McCarthy, Stephen G
; APPLICANT: Scallion, Bernard J
; APPLICANT: Snyder, Linda A
; TITLE OF INVENTION: NUCLEIC ACID VACCINES USING TUMOR ANTIGEN ENCODING NUCLEIC ACIDS
; TITLE OF INVENTION: CYTOKINE ADJUVANT ENCODING NUCLEIC ACID
; FILE REFERENCE: CEN310
; CURRENT APPLICATION NUMBER: US/10/247,703
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 69
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-247-703-69

Query Match 99.9%; Score 811; DB 12; Length 177;
Best Local Similarity 99.4%; Pred. No. 3.6e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 21 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 80
Qy 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFFQRSVPGHDNKMQPESSSY 120
Db 81 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIKOTKSDIIFFQRSVPGHDNKMQPESSSY 140
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 141 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 177

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Job time : 46 secs